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(54) Crystal structure (3 Å resolution) of the 30S ribosome and its use

(57) The invention provides an X-ray crystal structure of the 30S ribosome, obtained from *Thermus thermophilus* 30S subunit, having a tetragonal space group  $P4_2$  with unit cell dimensions of  $a = 401.4 \pm 4.0 \text{ Å}$ ,  $b = 401.4 \pm 4.0 \text{ Å}$ ,  $c = 175.9 \pm 5.0 \text{ Å}$ . An advantageous feature of the structure is that it diffracts beyond 3 Å reso-

lution. The invention also provides a crystal of 30S having the three dimensional atomic coordinates of the 30S ribosome, the coordinates being provided in Tables 1A and 1B. The data may be used for the rational design and modelling of inhibitors for the 30S ribosome, which have potential use as antibiotics.

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## Description

### Field of the Invention

- 5 [0001] The present invention relates to the provision of a high resolution crystal structure of the prokaryotic 30S ribosome subunit, and the use of this structure in drug discovery.

### Background of the Invention

- 10 [0002] The wealth of information made available through efforts in structural genomics and advances in computation has allowed structure-based drug design to emerge as a valuable tool in medicinal chemistry. In the past combinatorial chemistry, coupled with high-throughput approaches, shifted attention away from the more structure-based methods. Large-scale determination of protein structures is reversing the drug discovery process by starting with the protein structure and using it to identify and design new ligands. It is the integration of structure-based methods, virtual screening, and combinatorial chemistry that will provide the basis for more efficient drug design in the future, significantly reducing the time of the design cycle and the cost per marketed drug. Significant advances have already been made in AIDs, arthritis and cancer and in the treatment of hypertension e.g. captopril.

- 15 [0003] Translation of the genetic code occurs on the ribosome, a large nucleoprotein complex that consists of two subunits. In bacteria, the two subunits are denoted 30S and 50S. The 50S subunit contains the catalytic site of peptidyl transferase activity, while the 30S subunit plays a crucial role in decoding messenger RNA. Protein synthesis is a complex, multistep process that requires several extrinsic GTP-hydrolysing protein factors during each of the main stages of initiation, elongation and termination. Despite several decades of work, the molecular details of the process are poorly understood, and the elucidation of the mechanism of translation is one of the fundamental problems in molecular biology today. A recent collection of articles summarizes the state of understanding of the field [1].

- 20 [0004] A contribution to this problem was made by Yonath and coworkers, who after nearly a decade of work showed that structures as large as the 50S ribosomal subunit would form crystals that diffract beyond 3Å resolution [2]. Originally, it was not clear that phase information from such a large asymmetric unit could be obtained to high resolution, but the development of bright, tuneable synchrotron radiation sources, large and accurate area detectors, vastly improved crystallographic computing, and the advent of cryo-crystallography have all contributed to making structural studies of the ribosome more tractable. In our work, the use of anomalous scattering from the LIII edges of lanthanides and osmium has also played a critical role in obtaining phases.

- 25 [0005] The 30S ribosomal subunit (hereafter referred to as 30S) from *Thermus thermophilus* was originally crystallized by Trakhanov *et al.* in 2-methyl-2,4-pentanediol (MPD) [3] and soon afterwards by Yonath and coworkers in a mixture of ethylbutanol and ethanol [4]. Subsequent work by both groups showed that the MPD crystal form diffracted to about 9-12Å resolution [5, 6]. The diffraction limit of these crystals did not improve beyond 7Å resolution for almost a decade, but more recently both Yonath and coworkers [7, 8] and we [9] obtained crystals of the MPD form that exhibit significantly improved diffraction. However, unlike the crystals obtained by the Yonath group [8], our crystals do not require soaking in tungsten clusters or heat treatment in order to obtain high resolution diffraction.

- 30 [0006] We have previously described the structure of the 30S at 5.5Å resolution [9]. We were able to place all seven proteins whose structures were known at the time, infer the structure of protein S20 to be a three-helix bundle, trace the fold of an entire domain of 16S RNA, and identify a long RNA helix at the interface that contains the decoding site of the 30S. Proteins S5 and S7 were also placed in electron density maps of the 30S obtained by Yonath and coworkers.

- 35 [0007] The 30S ribosomal subunit is a major target for antibiotics. The ribosome is a useful target for antibiotics since the structure of the 30S is widely conserved between prokaryotes, allowing for broad spectrum antibiotics. However, resistance to current antibiotics is currently a major problem in the field of medicine. There are presently very few new antibiotics available which can be used to treat the highly resistant strains of bacteria such as MRSA (methicillin resistant *Staphylococcus aureus*) which are becoming increasingly widespread.

- 40 [0008] Understanding the interaction of antibiotics with the ribosome at the molecular level is important for two reasons. Firstly, antibiotics act by interfering with various aspects of ribosome function. Thus understanding their interaction will help shed light on mechanisms involved in translation. Secondly, a detailed knowledge of antibiotic interactions with the ribosome could aid the development of new drugs against increasingly resistant strains of bacteria. Although antibiotics were characterized several decades ago, a detailed knowledge of their mechanism will in general require a three-dimensional structure of their complex with the ribosome.

- 45 [0009] The low (greater than 3Å resolution) crystal structures described above do not provide sufficiently detailed resolution for useful modelling of the crystal structure of the 30S and there is thus a need for a high resolution structure which can be used usefully in the development of novel therapeutics.

Summary of the Invention

[0010] We have now solved and refined the structure of the 30S at 3Å resolution. The structure contains all of the ordered regions of 16S RNA and 20 associated proteins, and contains over 99% of the RNA sequence and 95% of the protein sequences, with the missing parts being exclusively at the termini of RNA or polypeptide chains. Here we describe the overall architecture and the main structural features of the 30S subunit.

[0011] The refined atomic resolution model of the 30S presented here allows the interpretation of a vast amount of biochemical data on its function in precise structural terms. The structure will also serve as a basis for the interpretation in molecular terms of lower resolution models of various functional states by electron-microscopy or x-ray crystallography. The 30S structure will help produce testable models for various aspects of ribosome function.

[0012] In a first aspect, the present invention provides a crystal of the *Thermus thermophilus* 30S subunit having a tetragonal space group  $P4_22$  with unit cell dimensions of  $a = 401.375 \text{ Å}$ ,  $b = 401.375 \text{ Å}$ ,  $c = 175.887 \text{ Å}$ , or more generally  $a = 401.4 \text{ Å}$ ,  $b = 401.4 \text{ Å}$ ,  $c = 175.9 \text{ Å}$ , but more preferably  $a = 401.4 \pm 4.0 \text{ Å}$ ,  $b = 401.4 \pm 4.0 \text{ Å}$ ,  $c = 175.9 \pm 5.0 \text{ Å}$ . An advantageous feature of the structure is that it diffracts beyond 3Å resolution. Another feature of the structure is that it was obtained in a method which did not involve soaking crystals in heavy atom (e.g. tungsten or tantalum) clusters or heat activation. Furthermore, it is specifically of the 885-888/910-912 base pairing confirmation of 16S RNA. These features, both singly and in combination all contribute to features of the invention which are advantageous.

[0013] In a second aspect, the invention also provides a crystal of 30S having the three dimensional atomic coordinates of the 30S ribosome. Table 1A provides a set of atomic coordinates of the 30S ribosome. Table 1B provides a set based upon the coordinates of Table 1A but which have been refined further from our data. Reference herein to "Table 1" is a reference to either of Table 1A or 1B (or where the context permits, both). Thus, for example, where it is stated that the invention refers to computer readable media with "atomic coordinate data according to Table 1 recorded thereon", this means that the media has either the data of Table 1A, or the data of Table 1B, or both, recorded thereon.

[0014] We have also observed that 30S crystals do not contain the S1 subunit protein. In our studies, we have found that by selectively removing this protein prior to crystallization, we have been able to obtain the improved resolution described herein. Although the atomic co-ordinates provided in Table 1 below allows those of skill in the art to bypass the need to undertake the crystallization of the 30S, this crystallization method nonetheless forms a further aspect of the invention.

[0015] Accordingly, there is provided a method for crystallizing a the 30S subunit to obtain a high resolution structure of a 30S subunit, which method comprises providing a 30S subunit, selectively removing the 31 subunit therefrom and crystallizing the 30S.

[0016] In a further aspect, the present invention provides a method for identifying a potential inhibitor of the 30S comprising the steps of:

- a. employing a three-dimensional structure of 30S, or at least one sub-domain thereof, to characterise at least one active site, the three-dimensional structure being defined by atomic coordinate data according to Table 1; and
- b. identifying the potential inhibitor by designing or selecting a compound for interaction with the active site.

[0017] In a further aspect, the present invention provides computer readable media with either (a) atomic coordinate data according to Table 1 recorded thereon, said data defining the three-dimensional structure of 30S or at least one sub-domain thereof, or (b) structure factor data for 30S recorded thereon, the structure factor data being derivable from the atomic coordinate data of Table 1.

Description of the Drawings.

[0018]

Figure 1 shows the secondary structure of the 30S ribosome.

Figure 2 is Table 1A and 1B.

Detailed Description of the Invention.Definitions.

[0019] The term "sub-domain" includes the following:

- (a) and element selected from the following:

at least one complete element of secondary structure, i.e. an alpha helix or a beta sheet, or RNA helix, as described in the detailed description below;

a group of two or more such elements which interact with each other;

at least one subunit protein;

a subgroup of subunit proteins, for example a group which includes two or more proteins which are found to interact with each other;

any of the above, when being protein or element thereof being used in conjunction with all or part of the 16S RNA structure associated with said elements or proteins;

(b) a space of volume defining a region around any one particular atom of interest (e.g. an atom involved in binding to an antibiotic), the volume being less than the total volume of the tetragonal space of the complete crystal. For example, the coordinates of atoms in a volume of from about 500 to about 15,000 Å<sup>3</sup> may be selected and used for the present invention. Such a space may be a sphere having a diameter of from about 10 Å to about 30 Å, centred around a point of interest; and

(c) a collection of at least 10, e.g. at least 25 such as at least 50, more preferably at least 100, even more preferably at least 500 atoms and most preferably at least 1000 atoms defined by the coordinates of Table 1, wherein at least 2 of said atoms, and preferably at least 50% of said atoms of the collection are located within 50 Å of each other.

[0020] An "active site" of the 30S is any part of this structure involved in tRNA or mRNA binding, factor binding or translocation. This includes regions responsible for binding initiation factors, elongation factor G or release factors, regions which are target sites for regulation by co-factors, phosphorylation or acetylation, and regions responsible for interaction with the 50S ribosome. It also includes regions which change conformation during translocation or protein synthesis, particularly one or more of the 16S RNA helices 18, 27, 34 and 44.

[0021] Particular regions of the 30S include antibiotic binding regions. Other regions include the three tRNA binding sites, i.e. the aminoacyl (A), peptidyl (P) and (exit) E sites.

Other active sites are those which undergo movement during translocation of tRNAs from the A to P sites and the P to E sites. Regions further include any one of the subunit proteins S2 to S20 and THX, including any of the individually identified subunit proteins in the accompanying examples.

[0022] By "fitting", is meant determining by automatic, or semiautomatic means, interactions between one or more atoms of a potential inhibitor molecule and one or more atoms or binding sites of the 30S, and calculating the extent to which such interactions are stable. Various computer-based methods for fitting are described further herein.

[0023] By "root mean square deviation" we mean the square root of the arithmetic mean of the squares of the deviations from the mean.

[0024] "Computer readable media" refers to any media which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media such as floppy discs, hard disc storage medium and magnetic tape; optical storage media such as optical discs or CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

[0025] A "computer system" refers to the hardware means, software means and data storage means used to analyse the atomic coordinate data of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means and data storage means. Desirably a monitor is provided to visualise structure data. The data storage means may be RAM or means for accessing computer readable media of the invention. Examples of such systems are microcomputer workstations available from Silicon Graphics Incorporated and Sun Microsystems running Unix based, Windows NT or IBM OS/2 operating systems.

Table 1.

[0026] The coordinates of Table 1 provide a measure of atomic location in Angstroms, to a third decimal place. In order to use the information in these Tables for the purposes described herein as being aspects of the present invention, these coordinates may be varied by up to  $\pm 1.0$ , such as by up to  $\pm 0.7$ , preferably no more than up to  $\pm 0.5$  Angstroms, without departing from the scope of the invention.

[0027] Furthermore, varying the relative atomic positions of the atoms of the structure so that the root mean square deviation of the 16S RNA or S2-S20 protein backbone atoms is less than 1.5 Å (preferably less than 1.0 Å and more preferably less than 0.5 Å) when superimposed on the coordinates provided in Table 1 for these structures, will generally result in a structure which is substantially the same as the structure of Table 1 in terms of both its structural characteristics and potency for structure-based drug design of 30S ligands.

[0028] Thus for the purposes described herein as being aspects of the present invention, it is within the scope of the



Invention if: the Table 1 coordinates are transposed to a different origin and/or axes; the relative atomic positions of the atoms of the structure are varied so that the root mean square deviation of conserved residue backbone atoms is less than 1.5Å (preferably less than 1.0Å and more preferably less than 0.5Å) when superimposed on the coordinates provided in Table 1 for the conserved residue backbone atoms; and/or the number and/or positions of water molecules is varied. Reference herein to the use of the coordinates of Table 1 thus includes the use of coordinates in which one or more individual values of the Table are varied in this way.

[0029] Table 1 includes coordinates of two zinc ions, together with 202 other ions which are not identified, although, while not wishing to be bound by any one theory, are believed to be selected from cobalt and magnesium. Some or all of these ions may optionally be discarded from Table 1 when using the data. The table also lists the coordinates of a 26 amino acid peptide, Thx, as well as a 8 nucleotide fragment of mRNA, NNNUCU, designated as molecule X. Both the coordinates of both these molecules may likewise optionally be discarded, i.e. so that the coordinates of the 16S RNA and the proteins S2 to S20 alone are modelled and used in applications of the invention.

[0030] There are a few N- or C-terminal sequences of the S2 to S20 proteins which were not resolved in the structure of Table 1, together with a some of the 5' and 3' residues of the 16S RNA. These are not essential for the purposes of the present invention, but are listed in Table 2 for completeness. Those of skill in the art may, if desired, wish to adapt the structures provided by the coordinate of Table 1 by modelling in one or more of the amino acids or nucleotides of Table 2.

[0031] This methodology provides those of skill in the art a means to provide 30S crystals of *T. thermophilus*. The conservation of ribosome structure, particularly regions of structure essential for function, between prokaryotes, for example prokaryotes which are human pathogens, such as *Staphylococcus* spp, and the like, allows the structure herein to be useful in the provision of anti-bacterial agents in general. Thus, the structure may be used to solve 30S subunits by the technique of molecular replacement. In such a method, x-ray diffraction data are obtained from crystals of a 30S subunit from another species, e.g. a species of a bacteria pathogenic to humans. The coordinates of Table 1 may be used to find the orientation of the unknown molecule in the crystal, and electron density maps calculated. These maps can then be interpreted with the sequence of the species in question, and the coordinates of our 30S structure can be used to help and speed interpretation. In this way, the structure of our 30S facilitates the determination of structures of 30S subunits and whole ribosomes from other organisms.

[0032] Accordingly, the invention provides a method for the determination of the structure of a bacterial 30S from a species other than *T. thermophilus* which method comprises:

- (a) crystallising the 30S of said species to obtain a crystal;
- (b) performing X-ray crystallography on said crystal to obtain X-ray diffraction data;
- (c) providing the structure data of Table 1; and
- (d) using molecular replacement to calculate an electron density map of the 30S.

[0033] In such a method the 30S may be prepared by removal of the S1 subunit, as described herein.

[0034] The electron density map obtained may then be used to calculate the atomic coordinate data of the 30S. The atomic coordinate data thus obtained may be used to for the design and analysis of new and specific ligands for 30S as described herein.

#### *The 30S crystal structure.*

[0035] The high resolution structure provided herein provides a crystal with unit cell dimensions which are provided in the accompanying table to 3 decimal places, i.e.  $a=b=401.375$ ,  $c=175.887$  Å. However, those of skill in the art wishing to reproduce the crystallization described herein and obtain such crystals will appreciate that a degree of experimental variability and error will mean that crystals of the invention will be obtained with a unit cell dimension within, but not exactly corresponding to, this size. Thus crystals of the invention may generally be defined as having unit cell dimensions of  $a=401.4 \pm 4.0$  Å,  $b=401.4 \pm 4.0$  Å,  $c=175.9 \pm 5.0$  Å, preferably  $a=401.4 \pm 1.0$  Å,  $b=401.4 \pm 1.0$  Å,  $c=175.9 \pm 2.0$  Å, preferably  $a=401.4 \pm 0.7$  Å,  $b=401.4 \pm 0.7$  Å,  $c=175.9 \pm 1.4$  Å, and more preferably  $a=401.4 \pm 0.2$  Å,  $b=401.4 \pm 0.2$  Å,  $c=175.9 \pm 0.4$  Å. These unit cell sizes are believed to define a novel and more highly resolved unit cell size than has previously been possible in the art.

#### *Production of crystals.*

[0036] To obtain crystals according to the present invention, we have found that selective removal of the S1 subunit protein is advantageous. A suitable method for the selective removal of the S1 subunit protein is by the use of a hydrophobic interaction chromatography column (poros-ET). 30S ribosomal subunits lacking the S1 subunit may suitably be separated from those containing the S1 subunit by running a column using a reverse ammonium sulfate gradient

from 1.5M to 0.5M, with 20mM Hepes, pH 7.5, and 10mM acetate. The 30S subunits lacking S1 are eluted first, giving the first major peak. During elution of the 30S peak the ammonium sulfate concentration is maintained at a constant level. Once the 30S peak has eluted the ammonium sulfate concentration is then further reduced to elute the 30S + S1 fraction.

5 [0037] An alternative method for the selective removal of the S1 subunit protein is by preparative gel electrophoresis. Gel electrophoresis may suitably be carried out by first preparing and mixing a 3% acrylamide, 0.5% agarose cylindrical gel, and pouring this gel into a BioRad Prep Cell. 30S ribosomal subunits are then loaded onto the gel and continuously eluted as they emerge from the other end of the gel. The 30S fraction lacking the S1 subunit comes off first, giving the first major peak. The 30S + S1 fraction gives the trailing peak (or shoulder) and can be discarded.

10 [0038] Once the S1 is removed, the crystals may be formed, using suitable conditions. These include the use of 13-17% v/v methyl-2,4-pentenediol in the presence of 200-300 (e.g. about 250) mM KCl, 50-100 (e.g. about 75) mM ammonium chloride, 15-30 (e.g. about 15 or about 25) mM  $MgCl_2$  at a pH of 6.0 - 7.5 (e.g. about pH 6.3 - 6.7 such as pH 6.5) in 50 - 150 (e.g. about 100) mM sodium or potassium cacodylate or MES (2-(N-morpholino)ethane sulphonic acid).

15 [0039] In a particular aspect, the conditions may comprise the use of 250 mM KCl, 75 mM  $NH_4Cl$ , 25 mM  $MgCl_2$ , 6 mM 2-mercaptoethanol in 0.1 M potassium cacodylate or 0.1 M MES (2-N-morpholinoethanesulfonic acid) at pH 6.5 with 13-17% MPD as the precipitant.

[0040] The crystals may be grown by any suitable method known as such to those of skill in the art. Suitably, the crystals may be grown over a period of 4-8 weeks at about 4°C. The structure of the crystals so obtained may be resolved, and crystals which resolve to a resolution of at least 3Å selected. Crystals which resolve to a resolution of at least 3Å obtainable by such a method are a further aspect of the invention.

#### Use of structure of Table 1.

25 [0041] The determination of the three-dimensional structure of 30S provides a basis for the design of new and specific ligands for 30S. For example, knowing the three-dimensional structure of 30S, computer modelling programs may be used to design different molecules expected to interact with possible or confirmed active sites, such as binding sites or other structural or functional features of 30S.

30 [0042] The high resolution model of the 30S provided by Table 1 may be used to examine and determine the binding of antibiotics known to target this ribosome subunit. Such antibiotics include paromomycin, streptomycin, spectinomycin, tetracycline, pactamycin and hygromycin B.

[0043] A candidate ligand, particular one which acts as an inhibitor molecule may be any available compound. A number of commercial sources of libraries of compound structures are available, for example the Cambridge Structural Database.

35 Such libraries may be used to allow computer-based high throughput screening of many compounds in order to identify those with potential to interact with the active site of a ribosome.

[0044] More specifically, a potential ligand capable of modulating 30S activity can be examined through the use of computer modelling using a docking program such as GRAM, DOCK, or AUTODOCK (see Walters et al., *Drug Discovery Today*, Vol.3, No.4, (1998), 160-178, and Dunbrack et al., *Folding and Design*, 2, (1997), 27-42) to identify potential ligands of 30S. This procedure can include computer fitting of potential ligands to 30S or a subdomain thereof to ascertain how well the shape and the chemical structure of the potential ligand will bind to the enzyme.

40 [0045] Also computer-assisted, manual examination of the active site structure of 30S may be performed. The use of programs such as GRID (Goodford, *J. Med. Chem.*, 28, (1985), 849-857) - a program that determines probable interaction sites between molecules with various functional groups and the enzyme surface - may also be used to analyse the active site to predict partial structures of ligands for the site.

45 [0046] Computer programs can be employed to estimate the attraction, repulsion, and steric hindrance of the two binding partners (e.g. the 30S and a potential ligand). Generally the tighter the fit, the fewer the steric hindrances, and the greater the attractive forces, the more potent the potential ligand since these properties are consistent with a tighter binding constant. Furthermore, the more specificity in the design of a potential ligand, the more likely it is that the ligand will not interact with other proteins as well. This will tend to minimise potential side-effects due to unwanted interactions with other proteins.

50 [0047] Having designed or selected possible binding ligands, these can then be screened for activity. Consequently, the method preferably further comprises the further steps of:

55 obtaining or synthesising the potential ligand; and  
contacting the potential ligand with 30S to determine the ability of the potential ligand to interact with 30S.

[0048] More preferably, in latter step the potential ligand is contacted with 30S under conditions to determine its

function, for example in a cell free translation system.

[0049] Instead of, or in addition to, performing such an assay, the method may comprise the further steps of:

obtaining or synthesising said potential ligand;

forming a complex of 30S and said potential ligand; and

analysing said complex by X-ray crystallography to determine the ability of said potential ligand to interact with 30S. Detailed structural information can then be obtained about the binding of the potential ligand to 30S, and in the light of this information adjustments can be made to the structure or functionality of the potential ligand, e.g. to improve binding to the active site. Steps c. to e. may be repeated and re-repeated as necessary.

[0050] Another aspect of the invention includes a compound which is identified as an ligand of 30S by the method of the above aspects of the invention.

[0051] The present high resolution structure of 30S provides a means to determine the location of binding of antibiotics, as well as the interactions at the location between 30S and the antibiotic. Such antibiotics include paromomycin, streptomycin spectinomycin, tetracycline, pactamycin and hygromycin B. The high structure of Table 1 may be used to model the binding to 30S of these, other antibiotics and other ligands. Thus in another aspect, the invention provides a method of analysing a 30S-ligand (wherein "ligand" includes an antibiotic) complex comprising the steps of (i) co-crystallising the 30S with the ligand or soaking the ligand into crystals of the 30S; (ii) collecting X-ray crystallographic diffraction data from the crystals of the 30S-ligand complex and (iii) using the three-dimensional structure of 30S of Table 1, or at least one sub-domain thereof, to generate a difference Fourier electron density map of the 30S-ligand; and (iv) modelling the ligand in the difference Fourier electron density.

[0052] Therefore, 30S-ligand complexes can be crystallised and analysed using X-ray diffraction methods, e.g. according to the approach described by Greer et al., *J. of Medicinal Chemistry*, Vol. 37, (1994), 1035-1054, and difference Fourier electron density maps can be calculated based on X-ray diffraction patterns of soaked or co-crystallised 30S and the solved structure of uncomplexed 30S. These maps can then be used to determine the structure of the ligand bound to the 30S and/or changes the conformation of 30S.

[0053] Data obtained from a ligand bound to 30S may be used to improve the ligand, for example by adding or removing functional groups, substituting groups or altering its shape to obtain improved candidates, which may then be screened, solved in complex as described herein above, in an iterative process.

[0054] Electron density maps can be calculated using programs such as those from the CCP4 computing package (Collaborative Computational Project 4. The CCP4 Suite: Programs for Protein Crystallography, *Acta Crystallographica*, D50, (1994), 760-763.). For map visualisation and model building programs such as "O" (Jones et al., *Acta Crystallography*, A47, (1991), 110-119) can be used.

[0055] By providing such computer readable media, the atomic coordinate data can be routinely accessed to model 30S or a sub-domain thereof. For example, RASMOL is a publicly available computer software package which allows access and analysis of atomic coordinate data for structure determination and/or rational drug design.

[0056] On the other hand, structure factor data, which are derivable from atomic coordinate data (see e.g. Blundell et al., in *Protein Crystallography*, Academic Press, New York, London and San Francisco, (1976)), are particularly useful for calculating e.g. difference Fourier electron density maps.

[0057] In another aspect, the present invention provides systems, particularly a computer systems, intended to generate structures and/or perform rational drug design for 30S or 30S ligand complexes, the systems containing either (a) atomic coordinate data according to Table 1, said data defining the three-dimensional structure of 30S or at least one sub-domain thereof, or (b) structure factor data for 30S, said structure factor data being derivable from the atomic coordinate data of Table 1.

[0058] Mutant strains resistant to the action of these antibiotics can arise through mutation of a protein subunit of the 30S or through mutation or modification in the 16S RNA (e.g. 2'O-methylation), or modification (e.g. acetylation) of the antibiotic). The sites of mutations in some cases are known or can be identified. Where such sites are identified through, for example, primary sequence data, the invention provides a means to model the structure of the mutants.

[0059] There is thus provided a method which comprises providing the structure of the 30S ribosome of Table 1, changing one amino acid or nucleotide of said structure to provide a mutant 30S, and modelling the structure of the mutant 30S to provide a structure of the mutant. The mutant may be used in the manner described above for the wild type, e.g. stored in computer readable form, modelled to provide ligands, and the like. The modelling may be based upon the predicted behaviour of the atoms of the changed amino acid based upon its interaction with the surrounding atoms in the model provided herein.

[0060] This process may be iterative, e.g. to produce successive mutations into the 30S structure, for example 2, 3, 4, or 5 to 10 mutations.

[0061] Regions of 30S which may be subject to this aspect of the invention include those regions identified in the accompanying examples as regions of the 30S involved in ribosome function.

[0062] In a further aspect, the present invention provides a means to solve or interpret electron density maps of the whole 70S ribosome at low or high resolution, and thus solve the structure of the whole 70S ribosome.

[0063] In particular, the invention provides a method for the determination of the structure of a bacterial 70S ribosome which method comprises:

- (a) crystallising the 70S of said species to obtain a crystal;
- (b) performing X-ray crystallography on said crystal to obtain X-ray diffraction data;
- (c) providing the structure data of Table 1; and
- (d) using molecular replacement to calculate an electron density map of the 70S.

[0064] The invention is illustrated below by the following examples, their accompanying Figures and Tables. In Table 1 there is shown in each row Atom number, element type, residue (amino acid, nucleotide, etc), number in molecule (for proteins N to C terminal direction, for nucleic acid 5' to 3' direction), X, Y and Z co-ordinates, occupancy, B factor ( $\text{\AA}^2$ ) and an identifier for the member of the 30S (e.g. for the subunits in the format "ASn" where A is an arbitrary letter, different for each member, S is the subunit and n is the subunit number; and for the 16S as "A16S").

[0065] Throughout the accompanying example, we use the numbering system for *E. coli* 16S RNA, as well as the standard helix numbering, denoted H1-H45, for the secondary structure elements [19] with some modifications as shown in Figure 1. The most significant differences between the *E. coli* and *T. thermophilus* sequences are a shorter H6 and H10, and insertions in H9 and H33a. Any insertions in *T. thermophilus* relative to *E. coli* are indicated in the coordinates with an insertion letter after the nucleotide number, following the practice for tRNA.

## **MATERIALS AND METHODS**

### *Crystallization of the 30S.*

[0066] Because we observed that the 30S crystals completely lacked ribosomal protein S1, care was taken to remove S1 selectively from the 30S prior to crystallization. Crystals were obtained in 13-17% MPD over a range of pH in the salt and magnesium conditions described by Trakhanov et al [3]. The crystals were largest and most reproducibly obtained at a pH of 6.5 in 0.1 M cacodylate or MES buffer. Crystals took approximately 6 weeks at 4°C to grow to their maximum size. The largest crystals, which were required for high resolution data collection, grew to a size of 80-100  $\square$  80-100  $\square$  200-300 microns. The activity of redissolved crystals in poly(U)-directed protein synthesis was comparable to that of freshly isolated 30S subunits.

### *Data collection.*

[0067] Crystals were transferred to 26% MPD by vapor diffusion in two steps over a period of 6 days. All crystals (except for those soaked in osmium hexammine or osmium pentammine) also contained 1 mM cobalt hexammine in the cryoprotectant. Crystals were flash-cooled by plunging into liquid nitrogen, and data collection was done in a cryostream at 90-100 K.

[0068] A large fraction of crystals was screened at beamlines 9.6 or 14.1 at the SRS at Daresbury Laboratories, using two short exposures at least 40 degrees apart. These crystals were then analyzed for diffraction limits, cell dimensions and mosaic spread. Only crystals of similar cell dimensions and with reasonable mosaic spread were used for data collection.

[0069] Potential derivatives were screened on beamlines X25 at the NSLS at Brookhaven National Laboratory and BM-14 at the ESRF (Grenoble). Data to about 4.5 $\text{\AA}$  were obtained from X25. High resolution data were collected at SBC ID-19 at the APS in Argonne National Laboratory, and ID14-4 at the ESRF. In all cases, derivative data were collected at the peak of the fluorescence at the LIII edge to maximize anomalous differences. At X25 and SBC ID-19, the kappa goniostat was used to rotate precisely about a mirror plane so that small anomalous differences could be measured accurately. Each crystal typically yielded 3-10 degrees of data. Data were integrated and scaled using HKL-2000 [10].

### *Structure determination.*

[0070] Previously determined phases at 5.5  $\text{\AA}$  [9] were used to locate heavy atom sites using anomalous difference Fourier maps. Initially, these sites were used for phasing to 3.35  $\text{\AA}$  using the program SOLVE [11], followed by density modification with SOLOMON [12], using the procedure implemented in SHARP [13]. Optimization of the various parameters in the procedure was required to obtain interpretable maps. The RNA and some of the proteins were built using the SOLVE maps. The sequence of *Thermus thermophilus* 16S RNA [14] was used for the structure. For proteins,

a combination of previously published sequences and new ones from the Göttingen *Thermus* genome sequencing project were used. Improved maps were obtained by calculating experimental phases to 3.2Å using SHARP followed by density modification and phase extension to 3.05Å with DM [15]. The improved maps allowed us to build all the ordered parts of the structure. The model was built using O [16], and refined using the program CNS [17]. Maximum likelihood refinement was used, initially with both amplitudes and experimental phase probability distributions to 3.35Å, and subsequently with amplitudes to 3.05Å.

## RESULTS

[0071] The 30S subunit from *Thermus thermophilus* consists of a 1522 nucleotide 16S ribosomal RNA [14] and 21 associated proteins, of which 20 have known counterparts in *E. coli*. Protein S21 is not present in *Thermus*, and protein S1 has been removed from the 30S prior to our crystallization. In addition, a 26 residue peptide, Thx, is present in *Thermus* 30S subunits [18].

[0072] Experimentally phased maps clearly showed main chain density for RNA and protein, individual bases (which were often of sufficient quality to distinguish purines from pyrimidines), and large well-ordered side chains of proteins. These maps were used to build 16S RNA and the previously unknown proteins S2, S3, S9, S10, S11, S12, S13, S14 and Thx. In addition, regions that were disordered in isolated structures or had changed significantly were also built. This often consisted of significant portions of the N- and C-terminal tails of the proteins, sometimes including entire domains that were unfolded in isolation. Proteins with small cores and long loops, such as S16 and S17, had to be substantially rebuilt, since these loops were generally disordered in the solution NMR structures. Finally, the entire structure was rebuilt after an initial round of refinement. Our current model consists of nucleotides 5-1511 of *Thermus thermophilus* 16S RNA (corresponding to 5-1534 of *E. coli* 16S RNA) and all of the ordered regions of the associated 20 proteins. The current model has been refined against 3.05 Å data with a conventional R-factor of 0.213, a free R-factor of 0.256 and good geometry. For the proteins, 94% of the residues were in the core or allowed regions of the Ramachandran plot, 3.9% in the generously allowed region and 1.8% in the disallowed region.

## 16S RNA

[0073] The secondary structure of 16S ribosomal RNA contains forty-five double helices connected by short single-stranded segments. In the crystal structure, many of these helices are coaxially stacked with a helix neighboring in the sequence. There are 13 groups of coaxially stacked helices and 23 unstacked helices in 16S rRNA, for a total of 36 helical elements. There are three different types of helix-helix packing. Most of the helical elements are packed in a minor groove to minor groove fashion, which often requires distortions from canonical A-form helical geometry in one of the two helices. Adenosines from internal loops or from hairpin loops often mediate docking against an A-form double helix, with a dense network of base-2' OH and 2' OH - 2' OH hydrogen bonds stabilising the packing. Less often, helix-helix packing occurs in a different mode, by insertion of a ridge of phosphates into a complementary minor groove of another helix. This packing mode is stabilized by hydrogen bonds between the ridge of phosphate oxygens and a layer of 2' OH and guanine base NH<sub>2</sub> groups. These guanine N2 groups are often made more accessible by the geometry of G-U pairs, which places this moiety farther into the minor groove than do Watson-Crick pairs. Finally, the rare end-on mode of interhelical packing uses a purine base to mediate the perpendicular packing of one helix against the minor groove of another helix. All three modes of helix-helix packing are further stabilized by idiosyncratic interactions between double-helical RNA and short non-helical RNA segments. Small bulges of one to three nucleotides are often found to pack either between helices or in the major groove of a helix.

### The 5' domain (fpd).

[0074] The fpd of 16S RNA contains 19 double helices, arranged as 7 groups of coaxially stacked helices and 5 unstacked helices, for a total of 12 double-helical elements packed tightly together. The result is a wedge-shaped mass of RNA that tapers to a single layer of double helices near the top of the domain. Like the other domains, the fpd is rather longer along the subunit interface than in the perpendicular direction.

[0075] The fpd can be divided into three subdomains, roughly corresponding to the upper, lower, and middle thirds of the secondary structure of the fpd. These subdomains make up the top and left-hand, the middle, and the lower right-hand sides of the body, respectively, in the view from 50S. The upper subdomain is a nearly planar arrangement of four helical elements (H16/H17, H4/H15, H1/H3, and H18). The H16/H17 stack forms the left-hand border of the body as viewed from 50S. This stack is almost 120 Å long, with H16 making contact with the head and H17 reaching the bottom of the subunit. Internal loops in both helices contain S-turns, which are used to modulate the position of the phosphate backbone in the case of H17, or to create an extended minor groove surface for helix-helix docking in the case of H16. The H4/H15 stack points towards the bottom of the subunit, with H15 well-packed against H17. The H1/H3

stack is bent by the conserved bulge at position 31, which results in the proximal end being horizontal and the terminal end pointing up to the head. The fourth helical element is H18, which is sharply bent to accommodate the 530 pseudoknot, defined by the unstacked helices 505-507/524-526 (H18.2) and 521-522/527-528 (H18.1). H18 is well-packed between the other two upwards-pointing elements of the upper subdomain, H1/H3 and H16. The 530 pseudoknot packs against the central pseudoknot at the H18.1 - H1 interface.

[0076] The middle subdomain contains four helical elements (H5, H6, H12/H6A, and H13/H14) that form a layer between the upper and lower subdomains in the centre of the body. There are relatively few packing interactions within the subdomain, and several of its helices pack against the upper subdomain on one side and the lower subdomain on the other. Thus at the bottom of the subunit, the conserved root of H6 packs against H8 (lower subdomain) on one side and H15 (upper subdomain) on the other side. Similarly, the H12/H6A stack packs against H4 (upper subdomain) and H7 (lower subdomain). H12/H6A also packs against H5 and the 117 loop, which pack against elements from the upper and lower subdomains, respectively. H5 is well-packed against H15 and the 117 loop stacks with the root of H11. H5 also packs against the H13/H14 stack in the phosphate ridge-minor groove manner. H13/H14 interacts with two different regions of the lower subdomain. The conserved UACG hairpin loop at the end of H14 packs against the 160 GAAA hairpin from H8 while the large conserved hairpin at the end of H13 interacts with H7. This hairpin loop also makes many interactions with elements from the middle subdomain.

[0077] The lower subdomain is a collection of three helical elements that form an open saddle-shaped structure in the lower right-hand corner of the body. The H8/H9 stack stretches from the back of the subunit to the front, with the conserved 160 GAAA hairpin pointing toward the 50S subunit. It packs tightly against the H7/H10 stack at the 4-way junction that joins them, and again at a Thermus-specific interaction between insertions at nucleotides 190 and 129. The H7/H10 stack also makes weak interactions with H15 and H17 from the upper subdomain at the bottom of the subunit. H11 contains two sharp bends that allow its conserved terminal hairpin loop to pack against H7. Both bends are stabilized by short-range minor-groove to minor-groove packing contacts.

#### 25 *The central domain (cd).*

[0078] The cd is the RNA component of the platform. Its fold based on our previous 5.5 Å structure [9] is in excellent agreement with our current structure. It contains nine helical elements folded into a W-shape in the 50S view. Two long single-stranded segments of RNA, the 570 and 820 loops, are also important structural elements. The domain is dominated by the long stack of H21/H22/H23, which forms the U-shaped perimeter of the domain. H21 is the only component of the left-hand arm of the W, while H22 and H23 form the base of the right-hand side. The right-hand arm of the W consists of H23B and H24A whose conserved hairpin loops are tightly packed. This arrangement requires sharp bends between H23 and H23B, and between H24 and H24A. The H23/H23B bend is stabilized by short-range minor groove-minor groove packing interactions. The H24/H24A bend is more unusual in that the bend is towards the major groove, which places a ridge of H24A phosphates in the major groove of H24. This major-groove bend is stabilized partly by short-range base-base and base-backbone interactions in the major groove of the bend, and partly by long-range interactions between the bent H24/H24A minor groove and the minor groove of H23. The heart of the central domain is the thicker middle arm of the W, which contains six helical elements (H20, H19/H25, H24, H26/H26A, H27, and H23B) and the 570 and 820 loops. On the left-hand side of the arm, the H26/H26A stack packs tightly against H22, the base of H25, and the 570 loop. The H25/H19 stack packs well with H20 and with the 570 loop. On the right-hand side of the central arm of the W, H23A packs well with H22, the 820 loop stacks on H24, and H24 packs well with the conserved GCAA hairpin loop of H27. In the centre of the arm, H23A packs with H26 in the phosphate ridge-minor groove manner, and the conserved H23A GAAG hairpin loop packs against H20. The 820 loop also interacts with H20, H25, and the 570 loop.

#### 45 *The 3' major domain (tmd).*

[0079] The 3' major domain (tpd) is the RNA component of the head of the 30S subunit. From the 50S view, the left-hand side of the head tapers to a beak made of RNA on the 50S side and protein on the solvent side. Like the other hand side of the head, the tpd is relatively thin in the direction perpendicular to the intersubunit interface. The tpd consists of fifteen helical elements, most of which do not stack on a neighboring helix, in contrast to the extensive stacking of neighboring helices seen in the fpd and the central domain. The tpd can be divided into three subdomains, which correspond to the upper, middle, and lower portions of the tpd secondary structure. The upper subdomain is an extended structure in the part of the head farthest from the 50S subunit, and makes relatively few packing contacts with RNA from the other head subdomains. The lower and middle subdomains are more globular and are more intimately packed together, and make up the front-right and front-left portions of the head, respectively. The middle subdomain includes the RNA portion of the beak.

[0080] The upper subdomain contains three helical elements that make up a well-separated structure on the solvent

side of the head. The subdomain is dominated by the H35-H36-H38-H39 stack, which stretches from the top to the bottom of the head. The other two helical elements of this subdomain are H37 and H40, which pack well with each other and loosely with the H35-H36-H38-H39 stack. The H37-H40 pack is mediated by a semiconserved GAAA hp in H40 with adjacent G-C pairs in H37.

5 [0081] The smaller middle subdomain is extended and contains only four helical elements, H32, H33/H33A, H33B and H34. Two of these (H33/H33A and H33B) form the Y-shaped RNA component of the beak. The H33/H33A stack points to the left in the 50S view while H33B points to the right, with its terminal conserved GNRA hairpin loop packed against H32, the covalent connection between the beak and the lower subdomain. H32 in turn packs against the H33-H34 junction as well as the 980 loop in the lower subdomain. With the exception of a small packing interaction with H32, the irregular H34 makes only long-range and somewhat tenuous packing interactions. The first is with H31 in the lower subdomain, an unusually weak minor-groove to minor groove packing. The second interaction is an unusual end-on packing interaction with the minor groove of the H34/H35/H38 junction in the upper subdomain.

10 [0082] The lower subdomain contains almost half of the tpd RNA and contains seven helical elements (H28/H29, H30, H31/980 loop, H41, H41A, H42 and H43) intimately packed into a globular mass. Helices 42 and 43 are arranged in an approximately parallel fashion at the centre of the fold, and each interacts with at least three of the other helical elements. Helices 42 and 43 dock together by means of a minor-groove to minor-groove packing of their conserved hairpin loops. On the solvent side of the H42/H43 pair, H41 packs with both H42 and H43, while the terminal GCAA hairpin loop of H41A packs against H42. This arrangement requires a sharp bend between H41 and H41A, whose minor grooves pack against each other at the bend. The H43-H41 pack is made more extensive by an underwound A-rich internal loop in H41. On the 50S side of the central H42/H43 pair are H29, H30, H31 and the 980 loop. H43 is well-packed with H29 and makes weaker interactions with H30 and the 980 loop, while H42 is well-packed with H30 and the 980 loop. The H42-H30 pack is mediated by successive conserved G-A pairs at the base of H42. The H43-H29 pack is mediated by a conserved S-turn at the base of H43. An S-turn also mediates the packing of H42 with H41. H31 is a peripheral element of the subdomain, packing well only with H30, but also packs with H34 from the middle subdomain.

#### *The 3' minor domain.*

30 [0083] The 3' minor domain consists of just two helices at the subunit interface. H44 is the longest single helix in the subunit, and stretches from the bottom of the head to the bottom of the body. It projects prominently from the body for interaction with the 50S subunit. H45 is approximately perpendicular to H44, with its conserved GGAA hairpin loop packed against H44 and available for interaction with the large subunit.

#### **PROTEINS IN THE 30S AND THEIR INTERACTION WITH 16S RRNA**

35 [0084] The current structure includes all of the 30S proteins except S1. The proteins generally consist of one or more folded domains, about half of which were known from previous work on isolated proteins. However, nearly all of the proteins contain extended termini or loops which interact intimately with RNA and were disordered in the isolated structures. Although most of the proteins form intimate contacts with ribosomal RNA, there are also protein-protein interactions such as those seen in the S4-S5-S8 and S3-S10-S14 clusters.

#### *Proteins in the central domain (S18, S11, S8, S15).*

45 [0085] S18: S18 in the 30S consists of residues 19-88. It consists of two helices, and a third helical element formed by two short turns from different parts of the structure that stack end-to-end. These helices together form a hydrophobic core. The C-terminus interacts with S11.

50 [0086] S11: S11 is a new structure and consists of two helices packed against a sheet, a type of fold seen in many ribosomal proteins. The sheet packs against the minor groove of the 690 loop (H23), and has a C-terminal extension that interacts with the C-terminal extension of S18 and also with the 790 loop (H24). Thus S11 stabilizes folding of the platform, by binding to both H23 and H24 near the tip of the platform.

[0087] S8: S8 binds near the H20/H21/H22 three-way junction and makes extensive interactions with H21 and H25. We now have molecular details of these interactions. In particular, two loops from S8 (87-92 and 112-118) wrap around the bulged bases 641-642 which were known to be required for high affinity binding of S8 [20, 21]. The N-terminus of the protein also packs against the minor groove of the 825 stem (H25), thus helping the folding of the central domain. Residues K55 on S8 and 653 on RNA are next to each other as would be expected from crosslinking [22]. The extension in Thermus S8 of the loop 69-76 packs against S2 from a symmetry related molecule.

55 [0088] S15: S15 binds between H20 and H22 near the three-way junction.

*The 5' domain binding proteins S17, S16 and S20.*

[0089] S17: Although originally thought to be exclusively a 5' domain binding protein, S17 also binds near the H20/H21/H22 three-way junction. The core of S17 is known from NMR to be a  $\beta$ -barrel with an OB fold, with long extended loops [23]. These loops are disordered in solution but bind RNA in the 30S. In Thermus, there is a long C-terminal extension to S17 that is organized as an RNA-binding helix. The core of the protein and the C-terminal helix make extensive contacts with H11 and also contact H7. The C-terminal helix also contacts H21 in the central domain. Two long loops, loop 1 (26-36) and loop 2 (60-71) are ordered and interact with disparate domains of RNA exactly as predicted. Loop 1, which contains the site of neamine resistance, is inserted between H21 and a highly irregular structure at the base of H11. The very tip of loop 1 also touches the 560 loop of 16S RNA. Loop 2, which contains the site of a mutant defective in assembly, is involved in stitching together H7 and H11. Thus S17 interacts with H7, H11 and the 560 loop in the 5' domain, and H21 in the central domain.

[0090] S16: For a small protein, S16 has an extensive footprint throughout the 5' domain. All of the residues (1-88) are visible in the electron density, and were rebuilt using an NMR structure [24] as a guide. The protein consists of an N-terminal sheet with two extended loops, and two short helices in the C-terminal end. All of the extensive contacts with 16S RNA are now clear. The  $\beta$ -sheet is packed between the 608/620 internal loop of H21 on one side and a minor groove of H4 on the other. The two loops that extend out from this sheet both interact with RNA. Loop 1 interacts with phosphates in major groove of H4, while residues 39-43 in loop 2 make contact with the phosphate backbone around the internal loop near 453 in H17. The first helix (53-61) also extends across the major groove of this internal loop, while the C-terminal end of the second helix along with the turn leading out of it point into a minor groove of H17. There is also interaction with the 110 loop of the 5' domain. Finally, the extended C-terminus lies across the minor groove at the tip of H17.

[0091] S20: The current high resolution structure of S20 shows that the long N-terminal helix contacts the base of H6 and the tip of helix 44, and many conserved basic residues make salt-bridges with phosphates. Helices 2 and 3 of S20 interact with the minor groove of H9, and helix 3 also interacts with tip of H11 (263). Finally the extreme C-terminus of the protein is extended and lies along the minor groove of H9, which is longer in Thermus by 11 nucleotides. Thus S20 brings together several helices near the bottom of the subunit.

*Proteins near the functional centre.*

[0092] S4, S5 and S12 are clustered near the "functional center" of the ribosome and contain the sites of several important mutations.

[0093] S4: In the structure of isolated S4 [25, 26] the N-terminal domain was cleaved off prior to crystallization. This N-terminal region is organized as a tightly folded domain with a metal ion (presumably zinc) that is coordinated by four cysteines. The domain is packed against the body of the protein. While the N-terminus of S4 is highly conserved, the cysteines themselves are not. It is therefore likely that the addition of a "zinc finger" is for additional stability rather than essential for the fold. The linker residues 46-52 connect the N-terminal domain with the rest of the protein. All domains of S4 make intimate contacts with RNA. In particular, S4 makes extensive contacts with a five-way junction where H3, H4, H16, H17 and H18 come together in the 5' domain.

[0094] The N-terminal domain is packed against the 420 stem-loop (H16). The largely helical domain I is packed against a complicated region of RNA where H3 and the 507 bulge at the base of H18 come together. The remaining domain of S4 makes extensive contact with the minor groove of the base of H16. In addition, it also makes contact with the tip of the H21, which is itself packed against H4. This position is consistent with the large body of biochemical data on S4 binding to 16S RNA.

[0095] The C-terminus of S4 makes an extensive interface with S5. Most of the known mutations of S4 and S5 that confer the ram phenotype are located in this region [27, 28]. The interface consists of several highly conserved salt bridges, and some of the mutations break one or more of these interactions.

[0096] S5: The structure of S5 shows that the loop from residues 14-28 is folded back onto the body of the protein in the isolated structure, but is a fully extended  $\beta$ -hairpin in the 30S. Also, the C-terminus of S5, which is disordered in the isolated structure, is mainly helical and packs against a complicated surface of S8 formed by many different strands.

[0097] S5 interacts closely with a region of the ribosome where the head and the body come together. In the head, the extended H35/H36 helix packs against H28, which forms the neck of the 30S connecting the body with the head. The tip of H36 makes contact with H26a, H2 and the central pseudoknot in the body. Protein S5 has contacts throughout this region, thereby stabilizing the conformation of the head with respect to the body.

[0098] The C-terminal sheet of S5 makes extensive interactions with the major groove of the H1 and the central pseudoknot. The N-terminal domain binds to the major groove of H36, as does the base of the  $\beta$ -hairpin. The tip of the hairpin interacts with the phosphate backbone in H28 and is also very close to H34. Nucleotide 560 is very close to



K121 in agreement with crosslinking data.

[0099] Most of the extensive interactions with RNA occur via major grooves or phosphate backbone.

[0100] S12: S12 is unusual both for its structure and location. It is unique among the 30S proteins in being on the interface side of the subunit. Its central core consists of a  $\beta$ -barrel with an OB fold, a feature found in other proteins such as S17. This core binds together H18, the 530 stem loop (at the tip of H18), H3 and a part of H44 close to the decoding site. An unusual feature is a long extension that connects this core with a short helix at the N-terminus of the protein. This extension threads between the 560 loop and H12 on one side, and H11 on the other, to make contact with both S8 and S17 on the other side of the 30S.

[0101] S12 is also the only protein in the vicinity of the decoding site near 1492-1493 of RNA. It is the site of a number of functionally interesting mutations.

#### *The head proteins S7 and S9.*

[0102] S7: Protein S7, whose structure in isolation was previously known, is known to be crucial for the assembly of the head [29]. In our 30S structure, the entire sequence is visible, including the very basic N-terminus. S7 binds to a small but complex region of the tpd that encompasses two multiple-stem junctions at a corner of the head. The majority of the interaction surface consists of H29 tightly docked to the S-turn at the base of H43. This docking requires a tight turn at 1346, probably stabilized by S7 binding. Because S7 also makes interactions with H28, its primary surface of interaction encompasses all three of the helices around the H28/H29/H43 three-way junction. The very tight docking of H29 to H43 gives rise to a small region of very high negative charge density, which is bound by a surface of S7 with very high concentration of positive charge (mainly S7 helices 1 and 4).

[0103] The second important interaction surface is centred on the second multiple stem junction that S7 binds, the H29/H30/H41/H42 junction. In this junction, H30 and the base of H42 are tightly packed together, with a tight turn between them. An S-turn between helices 41 and 42 mediates packing of H41 and H42, which also have a tight turn between them. H41 also packs very tightly against H43. S7 makes contacts to the phosphate backbone of H41, stabilizing its packing with H43, and to residues around 1240 and 1298 where the tight bends occur in the H29/H30/H41/H42 junction. Contacts with U1240 are particularly intimate: the universally conserved bulge U1240 is deeply buried into a conserved hydrophobic pocket between the 35 and 115 loops of S7.

[0104] The  $\beta$ -hairpin is not tightly associated with 16S RNA, but probably fits tightly into the minor groove of the E-site tRNA. The structure is in rough agreement with a model of S7 binding to ribosomal RNA [30], but there are also significant differences, including the location of H43.

[0105] S9: S9 consists of a compact RNA-binding domain consisting of 2 helices packed against a 5-stranded sheet, with a third short helix at the C-terminal end of the domain. From this domain, there is a long 25 residue C-terminal tail that snakes into elements of the head RNA. S9 also interacts with S7 via a small hydrophobic patch.

[0106] The sheet of S9 makes extensive interactions with H38 and H39. It also has two loops that interact with the 1250 internal loop of H41. The short C-terminal helix interacts with 1177-1180 in H40.

[0107] The long C-terminal extension snakes between the H29-H43 junction on one side and the H38-H34 junction on the other to touch a portion of H31.

#### *The S3 S10 S14 cluster.*

[0108] These three proteins form a cluster on the rear left-hand of the head, as the protein portion of the beak. S3 is clearly stacked on top of the other two proteins, consistent with the order of assembly.

[0109] S14: S14 is bound in a crevice in the RNA and is mostly covered by S3 and S10. Almost the whole molecule contacts RNA, including helices H31, H32, H34, H38, and H43. A cross linked residue is in close proximity to the RNA 28.

[0110] S14 contains a zinc ion coordinated by four cysteines from a CXXC-X12-CXXC motif. This motif is structurally similar to that found in the first zinc finger in the glucocorticoid receptor. This zinc binding motif is not conserved among all bacteria, although many of the residues surrounding it are, suggesting perhaps that in other organisms the protein folds via a hydrophobic core.

[0111] S10: S10 is structurally very similar to the S6 fold, with two helices packed against a 4-stranded sheet. Two of the strands in this sheet are connected by a long  $\beta$ -hairpin that extends out from the sheet and is inserted right into the centre of the head RNA fold. The  $\beta$ -hairpin makes most of the contacts with RNA, including helices H31, H34 and H41. The two strands of the sheet pack into the shallow minor groove of H39, making contacts with backbone residues on both sides of the groove.

[0112] S3: S3 contains two domains, both consisting of two helices packed against a 4-stranded sheet, which is similar to several other ribosomal proteins. In addition to the domains there is an N-terminal tail (all of which is visible). The C-terminal 30 residues are poorly conserved and disordered in the structure.

[0113] RNA contact is made by the N-terminal tail and the C-terminal domain. The N-terminal tail fits into a major

groove of H34. The sheet in the C-terminal domain also packs against H34.

[0114] The N-terminal domain makes few if any contacts with the RNA, but is mainly involved with making protein contacts with S10 and S14.

## 5 S13 and S19.

[0115] S13 and S19 form a loose dimer at the very "top" of the interface side of the head, extending both above and closer to the 50S than any of the head RNA. In spite of their location in this flexible region, they are both relatively well-defined in the electron density. Except for the C-terminal tail of S13, which reaches into the head and almost touches  
10 the tail of S9, none of these proteins are in contact with any other of the proteins in the small subunit. Together with S12, S11 and S15, these are among the few proteins that surround the region of intersubunit contact.

[0116] S13: All 125 residues of S13 are visible in the structure. The N-terminus (about 60 residues) forms a compact domain consisting of three small helices. Of this domain, only a small loop is in contact with the RNA and the domain appears to be clinging to the subunit only by virtue of its highly extended C-terminal region. This region begins with a  
15 long, straight alpha-helix that creeps along the top of the 30S head towards S19. It interacts mainly with the 1300 loop and H42. At this point the polypeptide chain bends by about 90 degrees, and the rest of the protein is mostly lacking in any secondary structure. This extended region curves around H41 into the head where it is buried in the RNA about 50-60 Å from the globular, N-terminal domain. It contacts H30 in the head.

[0117] S19: S19 consists of 92 residues. An NMR structure of isolated S19 [31] showed a single globular domain consisting of a helix packed against a three-stranded sheet, in which residues 9-78 were ordered. In the 30S structure, residues 2-81 are visible in the electron density. The C-terminus of the protein points towards the interface side and may become ordered in the 70S complex. Like S13, most of the globular domain of S19 is well separated from the RNA, but here both the N- and C-terminal extensions to the globular domain, as well as the loops 68-73 and 34-39 make contacts with H42. The C-terminal extension, like S13, bends around the RNA, to contact H31 while the N-  
25 terminus reaches H42 some considerable distance away. Thus, S19 straddles a portion of the head of the 30S. The residues in S13 and S19 that were crosslinked 48 are adjacent to each other in the structure.

## S2.

[0118] Thermus S2 consists of 256 residues of which 7-235 are visible in our structure. The protein consists of a large central domain of about 200 residues that consists of a 5-stranded parallel sheet and four helices connecting them. Two helices that form a small coiled-coil motif protrude out of this domain. The protein is located on the back of the 30S at the interface between the head and the rest of the particle. While it is primarily regarded as a "head" protein, it also makes contacts with the central domain in our structure.

35

## Thx.

[0119] This small 26 residue peptide was isolated and characterized from Thermus ribosomes [18]. Thx fills a cavity formed by a number of different elements at the very top of the head. Residues 1-24 are visible in the electron density, of which 8-14 form a short helix, flanked by extended ends. It is surrounded by H42, the tip of H41, and the base of H41, while the bottom of the cavity is formed by the major groove of H43. The protein is highly basic, and there are extensive salt-bridges between these residues and phosphates of nearby RNA. Thus Thx stabilizes a number of different RNA elements that come close together near the top of the head.

## 45 FUNCTIONAL INSIGHTS FROM THE STRUCTURE OF THE 30S RIBOSOMAL SUBUNIT.

[0120] During translation of the genetic code, the 30S ribosomal subunit provides the framework for base-pairing between the anticodon of tRNA and the codon of mRNA, and discriminates between cognate and non-cognate tRNAs to ensure translational fidelity, in a process termed decoding. During translocation, the ribosome must move by precisely one codon relative to mRNA and the bound tRNAs. Both decoding and translocation involve "switches" in which precise conformational changes occur in the ribosome. The atomic resolution structure of the 30S subunit allows us to interpret the environment of the mRNA and tRNA binding sites in molecular terms. In one well-characterized example of a functional switch involved in accuracy, we are also able to determine the spatial arrangement of its elements, thus elucidating its architecture. The structure also suggests other possible switching elements in the 30S, and sheds light  
55 on the kinds of movements that might occur.

[0121] The ribosome contains three tRNA binding sites, designated A (aminoacyl), P (peptidyl) and E (exit), after their respective tRNA substrates. Each site is bipartite, located partly on the 30S ribosomal subunit and partly on the 50S subunit. The A- and P-site tRNAs bind with their aminoacyl acceptor ends on the 50S subunit, and with their

anticodon ends base-paired to adjacent mRNA codons on the 30S subunit. The E-site tRNA is bound in a similar orientation but it is not known whether the E-site tRNA is base-paired to the E-site mRNA codon. The 30S subunit also binds mRNA upstream and downstream of the A, P and E codons. During translation, incoming aminoacyl tRNA is delivered to the A-site as a ternary complex with EF-Tu and GTP. Discrimination of cognate from non-cognate tRNAs occurs in the A-site. It is thought that there is also a second "proofreading" discrimination step in the A-site after GTP hydrolysis by EF-Tu, which is needed to discriminate cognate from near-cognate tRNAs. The 30S P-site has a much higher affinity for tRNA, in order to maintain the reading frame.

[0122] There is one well-characterized conformational switch in the 30S subunit, the helix 27 accuracy switch [32]. Genetic and biochemical data support a model in which this switch may be part of a larger-scale conformational change that occurs between initial selection and proofreading of the A-site tRNA, or the switch may play a role in translocation.

[0123] Until recently, there has been a large disparity between the high resolution of the genetic and biochemical data that define the RNA components of the active sites of the 30S subunit, and the relatively low-resolution of the three-dimensional structures of ribosomes available. The present invention addresses this disparity. In combination with previous biochemical and other data, it is now possible to identify the detailed structure of 30S active sites. In addition, by superimposing the tRNA and mRNA coordinates from the known 7.8 Å 70S structure, it is now possible to infer many of the interactions between 30S active sites and tRNA/mRNA ligands.

[0124] With our complete and high resolution structure of the 30S subunit in hand, it is now possible to identify at the residue level the elements of the 30S subunit that interact with the anticodon stem-loop (ASL) of the A, P and E-site tRNAs and associated mRNA.

[0125] Identification of the precise boundaries of the A, P, and E sites in an unbiased fashion in a structure determined in the absence of cognate tRNA ligands would normally be problematic. As it happens, the P-site in the 30S structure is filled with a stem-loop of RNA corresponding to residues 75-95 (in the *E. coli* numbering system) from the end of the "spur" (H6) of a neighbouring molecule. (Henceforth the term "spur" will refer to the symmetry-related spur docked in the P-site, rather than the spur at the bottom of the same subunit). The spur appears to mimic P-site tRNA by a variety of criteria. The extent of the 30S interaction with the anticodon stem-loop (ASL) is in very good agreement with that determined by affinity measurements [33] and by hydroxyl radical footprinting [34]. Secondly, the conformation of the spur stem-loop is distorted in order to more closely resemble the canonical tRNA ASL conformation [35, 36]: a U-A base pair is broken so that the spur hairpin loop can approximate the conformation of a tRNA ASL, complete with a U-turn and stacked anticodon. Another indication that the spur is a mimic of a bound P-site tRNA ASL is that of the twelve hydrogen bonds between 30S and the spur, only one appears to be sequence-specific, in accordance with the lack of sequence conservation in tRNA anticodon stems. Finally, close contacts of the spur with 16S RNA are on the whole consistent with chemical protection data for P-site tRNA [37] and with the 34-C1400 UV-induced crosslink between tRNA and 16S RNA [38] (the analogous residues are stacked in the 30S crystal structure).

[0126] Yet another indication that the spur mimics a P-site tRNA ASL is that its "pseudo-anticodon" is base-paired to a triplet of nucleotides, a mimic of mRNA. A fourth nucleotide is also visible 5' to the pseudo-anticodon, in the E site. These pseudo-codon bases are clearly pyrimidines, and appear to be UCU from the base-pairing geometries, which are U-U, U-C, and U-U since the pseudo-anticodon is UUU. The origin of this "pseudo-message" is unclear, but it probably comes from the 3' end of 16S RNA, which ends with 5' U1542C1543U1544 3'. The last nucleotide of our 16S model is C1533, so that seven disordered nucleotides would span the 25Å gap between C1533 and U1541, which is clearly stereochemically feasible. Alternatively, it is possible that the 3' end of 16S RNA has been cleaved somewhere between C1533 and U1541 prior to or during crystallization. The presence of functional mimics of mRNA and P-site tRNA also explains why these crystals diffract relatively well: the P-site tRNA makes extensive contacts with both the head and the body of the 30S, thereby helping to lock the particle into a single conformation.

[0127] To ask how well pseudomessage and spur mimic mRNA and the ASL of tRNA, we have used the 7.8 Å resolution structure of the 70S ribosome with bound mRNA and tRNAs [39]. In that structure, two elements of 16S RNA were identified, H27 and H44. To avoid any possible bias in our interpretation of the spur as a mimic, only H27 and H44 were used to in the alignment to superimpose the 70S structures onto our 30S structure. Despite the relatively low resolution of the 70S structure used, a least-squares superposition of these two elements had a phosphate r.m.s. d. of only 2.3 Å. When the 70S elements are superimposed in this manner onto our 30S structure, we found that indeed, as expected, the P-site tRNA superimposes well onto the 30S spur, and the 30S pseudo-message corresponds to the P-site codon. In particular, the orientation of the spur stem-loop is very similar to the 70S P-site ASL, and there are no significant clashes between the 70S A- and E-site tRNAs and our 30S subunit when superimposed in this manner. It is clear that the spur and pseudo-message cannot be perfect mimics, however, because the pseudo-anticodon - codon helix consists of three pyrimidine-pyrimidine base pairs, which are about 2 Å narrower than Watson-Crick pairs. Thus it seems likely that the spur and its pseudo-message are good but not perfect mimics of P-site tRNA and P-site codon, respectively, and that the spur mimic model should explain many but perhaps not all features of P-site tRNA binding to the 30S. Moreover, the transformed A- and P-site tRNAs and A-site codon provides a useful landmarks for modeling the extent of the A- and E-sites of the 30S.

## The P-site.

[0128] The P-site spur contacts several discrete regions of 16S RNA, most of which have been implicated in P-site binding by biochemical experiments. Two proteins also participate in binding the P-site ASL, a possibly surprising result. Most of the contact surface lies between the minor groove of the spur stem and 16S RNA nucleotides 1338-1341, 1229-1230, and the C-terminal tails of proteins S13 and S9. There are many hydrogen bonds between the minor groove (i.e. the 2' OH and base groups) of spur residues C91, C92, and G78 and the minor groove surface of G1338-A1339. Only one of these hydrogen bonds appears to be sequence-specific (G78 N2 - A1339 N3). A contact from Lys 126 of S9 appears to help stabilize this minor-groove to minor-groove packing interaction. Both 1338 and 1339 have previously been implicated in P-site binding [37]. A second area of contact, nearly continuous with the first, is between the 16S 1229-1230 sugar-phosphate backbone and spur residues G77 and G78. This region of contact is extended by the C-terminal tail of S13, which seems to help glue the spur and the 1229-1230 area together. The other areas of contact are much more tenuous. One interaction is stacking of U82 on C1400, which rationalizes the ASL 34-C1400 uv-induced crosslink [38]. The other is a packing interaction between A790 and spur residues 88-89, with a single hydrogen bond present. A790 is a so-called class III site, that is it is protected by either tRNA or 50S subunits. From the spur interaction, it would thus appear that binding of either the 50S subunit or the P-site ASL stabilizes a contact between A790 N6 and the phosphate of 1498, i.e. a contact between the central and three-prime minor domains. Finally, if the pseudo-codon - pseudo-anticodon helix were a few Å wider, as it would be for a Watson-Crick-paired helix, it would make van der Waals contact with the base of G966. G966 has also previously been implicated as part of the P-site by chemical modification experiments and has also been identified as a one of the few guanines crucial for P-site binding [40].

[0129] The P-site codon is threaded through the major groove of the upper portion of helix 44, in a universally conserved region of 16S RNA. There appears to be a tight turn between nucleotides -1 and +1, that is, between the last E-site and the first P-site codon nucleotides. This tight turn is stabilized by a hydrogen bond to the N1/N2 groups of the conserved residue G926, a residue previously implicated as crucial for P-site binding [40]. Additional hydrogen bonds are seen between the 2'OH of +1 to the phosphate of C1498, and between the phosphate of +2 and the 2' OH of C1498. The phosphate of +2 also stacks on the base of C1498. The phosphate of +3 is within hydrogen-bonding distance of two conserved cytidine N4 groups, from C1402 and C1403. The +3 base also stacks on the sugar of C1400. Finally, it appears likely that there are several magnesium ions that may help stabilize the location of the P-site codon in the major groove of H44.

## The E-site.

[0130] The E-site is defined by the environment surrounding the 70S E-site tRNA superimposed onto our 30S structure, as described above. Unlike the A and P-sites, the E-site consists mostly of protein. Proteins S7 and S11 have a small interface that binds the minor groove of the E-site ASL. The highly conserved beta-hairpin of S7 extends this surface nearly to the bottom of the anticodon, and it is possible that the S7 beta-hairpin helps dissociate the E-site codon from the E-site anticodon. The RNA portion of the E-site makes only tenuous interactions with the E-site ASL. 16S nucleotides 1382 and 1383 may interact with residue 34 of the anticodon. The minor-groove surface of the conserved 16S residues 693 and 694 may interact with the minor-groove surface of the 37-39 residues of the E-site ASL.

## The A-site.

[0131] The A-site is rather wider and shallower than the P or E sites, perhaps in order to allow rotation of the A-site codon-anticodon helix during or after GTP hydrolysis by EF-Tu. The RNA components of the A-site appear to include portions of the 530 loop, H34 in the head, and residues 1492-1493 from the 3' minor domain, all of which have been previously implicated in A-site binding.

The Helix 27 switch.

[0132] It is clear that many of the elements that make contact with the various tRNA would have to move during translocation. Indeed, the ribosome is known to undergo extensive conformational changes during the elongation cycle, and these must involve breaking and making precise contacts. However, the precise switching elements in these conformational changes are not known in general, with the exception of a switch in H27.

[0133] H27 is proposed to have two alternative base-pairing schemes during translation, one a "ram" or permissive form that pairs 885-887 with 910-912, and an alternative "restrictive" form that pairs 888-890 with 910-912 [32]. The ram form appears to be the more stable form in the ribosome and it features an S-turn (or loop E motif) in H27. The S-turn in H27 is also seen in the tRNA-bound structure of the 70S [39]. A switch to the restrictive form would involve a sliding of the two strands of H27 relative to each other and the S-turn would be replaced by an internal loop with a

different structure for H27. Indeed, analysis of the two forms by cryoelectron microscopy reveal noticeable conformational changes in the ribosome, especially around the A-site [41]. We can now precisely define the structure around H27 and use previous chemical modification data [32] to suggest the kinds of movement involved.

[0134] The S-turn in H27 around 888 is right next to 1489 in H44, and H27 packs against the minor groove of H44 just below the decoding site. The tip of H27 is close to H11, while 885, which is base-paired with 910 in our conformation, is near both H1 and the 570 loop. Finally, 914 is near both H1 and 526 in the 530 loop. Thus H27 is right in the heart of an area which includes the decoding site and the 530 loop. So it is not surprising that a change in the conformation of H27 would have affect these elements.

[0135] A number of elements that are more accessible in the "restrictive" state appear to be protected in the structure of the present invention. Thus for example, 524-526 are currently base-paired with 507-505 in the 530 pseudoknot. This suggests that the 530 pseudoknot could be broken in the restrictive state. Similarly, 1053 and 1197 are base-paired in the current structure, but they are part of a distorted region of H34 analogous to an S-turn, and it is not hard to envisage that an analogous switch might occur in H34 in the alternative state. Thus the data in combination with our structure suggests that H34 in the head and the 530 loop in the shoulder move between the two states, with H34 possibly adopting an alternative form, and the 530 pseudoknot being disrupted. In this context, it is interesting to note that both H34 and the 530 loop have been implicated in tRNA binding.

[0136] Other parts of the chemical protection data, especially those that are supposed to indicate enhanced accessibility in the *ram* state, are not so easy to rationalize since they involve protected bases in our structure.

[0137] The 30S structure has allowed us to identify details of the tRNA and mRNA binding sites, as well as obtain our first detailed look at the structure around the H27 switch. Clearly, H27 is only one component of major conformational changes that occur during translation. Analysis of the high resolution 30S structure should allow us to identify other potential switching elements, which may then be tested genetically.

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- 40
- 45
- 50
- 55

TABLE 2

			REMARK 465	ILE B	5
		35	REMARK 465	THR B	6
5	REMARK 465 MISSING RESIDUES		REMARK 465	GLU B	241
	REMARK 465 THE FOLLOWING		REMARK 465	ALA B	242
	RESIDUES WERE NOT LOCATED IN		REMARK 465	GLU B	243
10	THE		REMARK 465	ALA B	244
	REMARK 465 EXPERIMENT.	40	REMARK 465	THR B	245
	(M=MODEL NUMBER; RES=RESIDUE		REMARK 465	GLU B	246
15	NAME; C=CHAIN		REMARK 465	THR B	247
	REMARK 465 IDENTIFIER;		REMARK 465	PRO B	248
	SSSEQ=SEQUENCE NUMBER;		REMARK 465	GLU B	249
20	I=INSERTION CODE.)	45	REMARK 465	GLY B	250
	REMARK 465		REMARK 465	GLU B	251
	REMARK 465 M RES C SSSEQI		REMARK 465	SER B	252
25	REMARK 465 U A 0		REMARK 465	GLU B	253
	REMARK 465 U A 1		REMARK 465	VAL B	254
	REMARK 465 U A 2	50	REMARK 465	GLU B	255
30	REMARK 465 G A 3		REMARK 465	ALA B	256
	REMARK 465 U A 4		REMARK 465	MET C	1
	REMARK 465 C A 1535		REMARK 465	ILE C	208
35	REMARK 465 C A 1536		REMARK 465	GLY C	209
	REMARK 465 U A 1537	55	REMARK 465	GLY C	210
	REMARK 465 C A 1538		REMARK 465	GLN C	211
40	REMARK 465 C A 1539		REMARK 465	LYS C	212
	REMARK 465 U A 1540		REMARK 465	PRO C	213
	REMARK 465 U A 1541		REMARK 465	LYS C	214
45	REMARK 465 U A 1542	60	REMARK 465	ALA C	215
	REMARK 465 C A 1543		REMARK 465	ARG C	216
	REMARK 465 U A 1544		REMARK 465	PRO C	217
50	REMARK 465 MET B 1		REMARK 465	GLU C	218
	REMARK 465 PRO B 2		REMARK 465	LEU C	219
	REMARK 465 VAL B 3	65	REMARK 465	PRO C	220
55	REMARK 465 GLU B 4		REMARK 465	LYS C	221



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	REMARK 465	ALA C	222		REMARK 465	MET J	1
	REMARK 465	GLU C	223	35	REMARK 465	PRO J	2
5	REMARK 465	GLU C	224		REMARK 465	VAL J	101
	REMARK 465	ARG C	225		REMARK 465	GLY J	102
	REMARK 465	PRO C	226		REMARK 465	GLY J	103
10	REMARK 465	ARG C	227		REMARK 465	GLY J	104
	REMARK 465	ARG C	228	40	REMARK 465	ARG J	105
	REMARK 465	ARG C	229		REMARK 465	MET K	1
15	REMARK 465	ARG C	230		REMARK 465	ALA K	2
	REMARK 465	PRO C	231		REMARK 465	LYS K	3
	REMARK 465	ALA C	232		REMARK 465	LYS K	4
20	REMARK 465	VAL C	233	45	REMARK 465	PRO K	5
	REMARK 465	ARG C	234		REMARK 465	SER K	6
	REMARK 465	VAL C	235		REMARK 465	LYS K	7
25	REMARK 465	LYS C	236		REMARK 465	LYS K	8
	REMARK 465	LYS C	237		REMARK 465	LYS K	9
	REMARK 465	GLU C	238	50	REMARK 465	VAL K	10
30	REMARK 465	GLU C	239		REMARK 465	MET L	1
	REMARK 465	MET D	1		REMARK 465	VAL L	2
	REMARK 465	MET E	1		REMARK 465	ALA L	3
35	REMARK 465	PRO E	2		REMARK 465	LEU L	4
	REMARK 465	GLU E	3	55	REMARK 465	ALA L	129
	REMARK 465	THR E	4		REMARK 465	LYS L	130
40	REMARK 465	GLU E	155		REMARK 465	THR L	131
	REMARK 465	ALA E	156		REMARK 465	ALA L	132
	REMARK 465	HIS E	157		REMARK 465	ALA L	133
45	REMARK 465	ALA E	158	60	REMARK 465	LYS L	134
	REMARK 465	GLN E	159		REMARK 465	LYS L	135
	REMARK 465	ALA E	160		REMARK 465	MET M	1
50	REMARK 465	GLN E	161		REMARK 465	MET N	1
	REMARK 465	GLY E	162		REMARK 465	MET O	1
	REMARK 465	MET G	1	65	REMARK 465	ALA P	84
55	REMARK 465	MET I	1		REMARK 465	ARG P	85

	REMARK 465	GLU P	86		REMARK 465	ALA T	2
5	REMARK 465	GLY P	87	35	REMARK 465	GLN T	3
	REMARK 465	ALA P	88		REMARK 465	LYS T	4
	REMARK 465	MET Q	1		REMARK 465	LYS T	5
10	REMARK 465	MET R	1		REMARK 465	PRO T	6
	REMARK 465	SER R	2		REMARK 465	LYS T	7
	REMARK 465	THR R	3	40	REMARK 465	LYS V	26
15	REMARK 465	LYS R	4		REMARK 465	LYS V	27
	REMARK 465	ASN R	5				
	REMARK 465	ALA R	6				
20	REMARK 465	LYS R	7				
	REMARK 465	PRO R	8				
	REMARK 465	LYS R	9				
25	REMARK 465	LYS R	10				
	REMARK 465	GLU R	11				
	REMARK 465	ALA R	12				
30	REMARK 465	GLN R	13				
	REMARK 465	ARG R	14				
	REMARK 465	ARG R	15				
35	REMARK 465	MET S	1				
	REMARK 465	GLY S	82				
	REMARK 465	HIS S	83				
40	REMARK 465	GLY S	84				
	REMARK 465	LYS S	85				
	REMARK 465	GLU S	86				
45	REMARK 465	ALA S	87				
	REMARK 465	LYS S	88				
	REMARK 465	ALA S	89				
50	REMARK 465	THR S	90				
	REMARK 465	LYS S	91				
	REMARK 465	LYS S	92				
55	REMARK 465	LYS S	93				
	REMARK 465	MET T	1				

## Claims

1. A crystal of a 30S subunit having a tetragonal space group  $P4_12_12$  with unit cell dimensions of  $a = 401.375 \text{ \AA}$ ,  $b = 401.375 \text{ \AA}$ ,  $c = 175.887 \text{ \AA}$ .
2. A crystal of a 30S subunit having a tetragonal space group  $P4_12_12$  with unit cell dimensions of  $a = 401.4 \text{ \AA}$ ,  $b = 401.4 \text{ \AA}$ ,  $c = 175.9 \text{ \AA}$ .
3. A crystal of a 30S ribosomal subunit having a resolution better (numerically less) than about  $3 \text{ \AA}$ .
4. A crystal a 30S ribosomal subunit having the structure defined by the co-ordinates of Table 1.
5. A computer-based method of rational drug design which comprises:
  - providing the structure of a 30S ribosomal subunit as defined by the coordinates of Table 1;
  - providing the structure of a candidate modulator molecule; and
  - fitting the structure of candidate to the structure of the 30S of Table 1.
6. A computer-based method for identifying a potential inhibitor of the 30S ribosome comprising the steps of:
  - a. employing a three-dimensional structure of 30S, or at least one sub-domain thereof, to characterise at least one active site, the three-dimensional structure being defined by atomic coordinate data according to Table 1; and
  - b. identifying the potential inhibitor by designing or selecting a compound for interaction with the active site.
7. The method of claim 6 which further comprises:
  - c. obtaining or synthesising the potential inhibitor;
  - d. contacting the potential inhibitor with 30S to determine the ability of said inhibitor to interact with the 30S.
8. The method of claim 6 which further comprises:
  - c. obtaining or synthesising said potential ligand;
  - d. forming a complex of 30S and said potential ligand; and
  - e. analysing said complex by X-ray crystallography to determine the ability of said potential ligand to interact with 30S.
9. A method for the determination of the structure of a bacterial 30S from a species other than *T. thermophilus* which method comprises:
  - (a) crystallising the 30S of said species to obtain a crystal;
  - (b) performing X-ray crystallography on said crystal to obtain X-ray diffraction data;
  - (c) providing the structure data of Table 1; and
  - (d) using molecular replacement to calculate an electron density map of the 30S.
10. A computer system, intended to generate structures and/or perform rational drug design for the 30S ribosome or complexes of the 30S ribosome with a potential modulator, the system containing either (a) atomic coordinate data according to Table 1, said data defining the three-dimensional structure of 30S or at least one sub-domain thereof, or (b) structure factor data for 30S, said structure factor data being derivable from the atomic coordinate data of Table 1.
11. A computer readable media with either (a) atomic coordinate data according to Table 1 recorded thereon, said data defining the three-dimensional structure of the 30S ribosome, at least one atom or at least one sub-domain thereof, or (b) structure factor data for the 30S ribosome recorded thereon, the structure factor data being derivable from the atomic coordinate data of Table 1.

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AT00	1501	CA	ALA	219	100.110	104.100	42.000	1.00	11.19	004
AT00	1502	CA	ALA	220	100.110	104.100	42.000	1.00	11.19	004
AT00	1503	CA	ALA	221	100.110	104.100	42.000	1.00	11.19	004
AT00	1504	CA	ALA	222	100.110	104.100	42.000	1.00	11.19	004
AT00	1505	CA	ALA	223	100.110	104.100	42.000	1.00	11.19	004
AT00	1506	CA	ALA	224	100.110	104.100	42.000	1.00	11.19	004
AT00	1507	CA	ALA	225	100.110	104.100	42.000	1.00	11.19	004
AT00	1508	CA	ALA	226	100.110	104.100	42.000	1.00	11.19	004
AT00	1509	CA	ALA	227	100.110	104.100	42.000	1.00	11.19	004
AT00	1510	CA	ALA	228	100.110	104.100	42.000	1.00	11.19	004

**1**

一、本行在各地設有分行及支行，凡有存款、放款、匯兌、買賣有價證券等業務，均極妥速辦理。

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ATON	2109	C	ALA	117	191.992	112.679	76.631	1.00	52.98	C23
ATON	2110	C	ALA	117	191.990	112.617	74.473	1.00	52.98	C23
ATON	2111	C	ALA	117	191.988	112.555	72.315	1.00	52.98	C23
ATON	2112	C	ALA	117	191.986	112.493	70.157	1.00	52.98	C23
ATON	2113	C	ALA	117	191.984	112.431	68.000	1.00	52.98	C23
ATON	2114	C	ALA	117	191.982	112.369	65.842	1.00	52.98	C23
ATON	2115	C	ALA	117	191.980	112.307	63.685	1.00	52.98	C23
ATON	2116	C	ALA	117	191.978	112.245	61.527	1.00	52.98	C23
ATON	2117	C	ALA	117	191.976	112.183	59.370	1.00	52.98	C23
ATON	2118	C	ALA	117	191.974	112.121	57.212	1.00	52.98	C23
ATON	2119	C	ALA	117	191.972	112.059	55.055	1.00	52.98	C23
ATON	2120	C	ALA	117	191.970	111.997	52.897	1.00	52.98	C23
ATON	2121	C	ALA	117	191.968	111.935	50.740	1.00	52.98	C23
ATON	2122	C	ALA	117	191.966	111.873	48.582	1.00	52.98	C23
ATON	2123	C	ALA	117	191.964	111.811	46.425	1.00	52.98	C23
ATON	2124	C	ALA	117	191.962	111.749	44.267	1.00	52.98	C23
ATON	2125	C	ALA	117	191.960	111.687	42.110	1.00	52.98	C23
ATON	2126	C	ALA	117	191.958	111.625	39.952	1.00	52.98	C23
ATON	2127	C	ALA	117	191.956	111.563	37.795	1.00	52.98	C23
ATON	2128	C	ALA	117	191.954	111.501	35.637	1.00	52.98	C23
ATON	2129	C	ALA	117	191.952	111.439	33.480	1.00	52.98	C23
ATON	2130	C	ALA	117	191.950	111.377	31.322	1.00	52.98	C23
ATON	2131	C	ALA	117	191.948	111.315	29.165	1.00	52.98	C23
ATON	2132	C	ALA	117	191.946	111.253	27.007	1.00	52.98	C23
ATON	2133	C	ALA	117	191.944	111.191	24.850	1.00	52.98	C23
ATON	2134	C	ALA	117	191.942	111.129	22.692	1.00	52.98	C23
ATON	2135	C	ALA	117	191.940	111.067	20.535	1.00	52.98	C23
ATON	2136	C	ALA	117	191.938	111.005	18.377	1.00	52.98	C23
ATON	2137	C	ALA	117	191.936	110.943	16.220	1.00	52.98	C23
ATON	2138	C	ALA	117	191.934	110.881	14.062	1.00	52.98	C23
ATON	2139	C	ALA	117	191.932	110.819	11.905	1.00	52.98	C23
ATON	2140	C	ALA	117	191.930	110.757	9.747	1.00	52.98	C23
ATON	2141	C	ALA	117	191.928	110.695	7.590	1.00	52.98	C23
ATON	2142	C	ALA	117	191.926	110.633	5.432	1.00	52.98	C23
ATON	2143	C	ALA	117	191.924	110.571	3.275	1.00	52.98	C23
ATON	2144	C	ALA	117	191.922	110.509	1.117	1.00	52.98	C23
ATON	2145	C	ALA	117	191.920	110.447	-1.040	1.00	52.98	C23
ATON	2146	C	ALA	117	191.918	110.385	-3.198	1.00	52.98	C23
ATON	2147	C	ALA	117	191.916	110.323	-5.355	1.00	52.98	C23
ATON	2148	C	ALA	117	191.914	110.261	-7.513	1.00	52.98	C23
ATON	2149	C	ALA	117	191.912	110.199	-9.670	1.00	52.98	C23
ATON	2150	C	ALA	117	191.910	110.137	-11.828	1.00	52.98	C23
ATON	2151	C	ALA	117	191.908	110.075	-13.985	1.00	52.98	C23
ATON	2152	C	ALA	117	191.906	110.013	-16.143	1.00	52.98	C23
ATON	2153	C	ALA	117	191.904	109.951	-18.300	1.00	52.98	C23
ATON	2154	C	ALA	117	191.902	109.889	-20.458	1.00	52.98	C23
ATON	2155	C	ALA	117	191.900	109.827	-22.615	1.00	52.98	C23
ATON	2156	C	ALA	117	191.898	109.765	-24.773	1.00	52.98	C23
ATON	2157	C	ALA	117	191.896	109.703	-26.930	1.00	52.98	C23
ATON	2158	C	ALA	117	191.894	109.641	-29.088	1.00	52.98	C23
ATON	2159	C	ALA	117	191.892	109.579	-31.245	1.00	52.98	C23
ATON	2160	C	ALA	117	191.890	109.517	-33.403	1.00	52.98	C23
ATON	2161	C	ALA	117	191.888	109.455	-35.560	1.00	52.98	C23
ATON	2162	C	ALA	117	191.886	109.393	-37.718	1.00	52.98	C23
ATON	2163	C	ALA	117	191.884	109.331	-39.875	1.00	52.98	C23
ATON	2164	C	ALA	117	191.882	109.269	-42.033	1.00	52.98	C23
ATON	2165	C	ALA	117	191.880	109.207	-44.190	1.00	52.98	C23
ATON	2166	C	ALA	117	191.878	109.145	-46.348	1.00	52.98	C23
ATON	2167	C	ALA	117	191.876	109.083	-48.505	1.00	52.98	C23
ATON	2168	C	ALA	117	191.874	109.021	-50.663	1.00	52.98	C23
ATON	2169	C	ALA	117	191.872	108.959	-52.820	1.00	52.98	C23
ATON	2170	C	ALA	117	191.870	108.897	-54.978	1.00	52.98	C23
ATON	2171	C	ALA	117	191.868	108.835	-57.135	1.00	52.98	C23
ATON	2172	C	ALA	117	191.866	108.773	-59.293	1.00	52.98	C23
ATON	2173	C	ALA	117	191.864	108.711	-61.450	1.00	52.98	C23
ATON	2174	C	ALA	117	191.862	108.649	-63.608	1.00	52.98	C23
ATON	2175	C	ALA	117	191.860	108.587	-65.765	1.00	52.98	C23
ATON	2176	C	ALA	117	191.858	108.525	-67.923	1.00	52.98	C23
ATON	2177	C	ALA	117	191.856	108.463	-70.080	1.00	52.98	C23
ATON	2178	C	ALA	117	191.854	108.401	-72.238	1.00	52.98	C23
ATON	2179	C	ALA	117	191.852	108.339	-74.395	1.00	52.98	C23
ATON	2180	C	ALA	117	191.850	108.277	-76.553	1.00	52.98	C23
ATON	2181	C	ALA	117	191.848	108.215	-78.710	1.00	52.98	C23
ATON	2182	C	ALA	117	191.846	108.153	-80.868	1.00	52.98	C23
ATON	2183	C	ALA	117	191.844	108.091	-83.025	1.00	52.98	C23
ATON	2184	C	ALA	117	191.842	108.029	-85.183	1.00	52.98	C23
ATON	2185	C	ALA	117	191.840	107.967	-87.340	1.00	52.98	C23
ATON	2186	C	ALA	117	191.838	107.905	-89.498	1.00	52.98	C23
ATON	2187	C	ALA	117	191.836	107.843	-91.655	1.00	52.98	C23
ATON	2188	C	ALA	117	191.834	107.781	-93.813	1.00	52.98	C23
ATON	2189	C	ALA	117	191.832	107.719	-95.970	1.00	52.98	C23
ATON	2190	C	ALA	117	191.830	107.657	-98.128	1.00	52.98	C23
ATON	2191	C	ALA	117	191.828	107.595	-100.285	1.00	52.98	C23
ATON	2192	C	ALA	117	191.826	107.533	-102.443	1.00	52.98	C23
ATON	2193	C	ALA	117	191.824	107.471	-104.600	1.00	52.98	C23
ATON	2194	C	ALA	117	191.822	107.409	-106.758	1.00	52.98	C23
ATON	2195	C	ALA	117	191.820	107.347	-108.915	1.00	52.98	C23
ATON	2196	C	ALA	117	191.818	107.285	-111.073	1.00	52.98	C23
ATON	2197	C	ALA	117	191.816	107.223	-113.230	1.00	52.98	C23
ATON	2198	C	ALA	117	191.814	107.161	-115.388	1.00	52.98	C23
ATON	2199	C	ALA	117	191.812	107.099	-117.545	1.00	52.98	C23
ATON	2200	C	ALA	117	191.810	107.037	-119.703	1.00	52.98	C23
ATON	2201	C	ALA	117	191.808	106.975	-121.860	1.00	52.98	C23
ATON	2202	C	ALA	117	191.806	106.913	-124.018	1.00	52.98	C23
ATON	2203	C	ALA	117	191.804	106.851	-126.175	1.00	52.98	C23
ATON	2204	C	ALA	117	191.802	106.789	-128.333	1.00	52.98	C23
ATON	2205	C	ALA	117	191.800	106.727	-130.490	1.00	52.98	C23
ATON	2206	C	ALA	117	191.798	106.665	-132.648	1.00	52.98	C23
ATON	2207	C	ALA	117	191.796	106.603	-134.805	1.00	52.98	C23
ATON	2208	C	ALA	117	191.794	106.541	-136.963	1.00	52.98	C23
ATON	2209	C	ALA	117	191.792	106.479	-139.120	1.00	52.98	C23
ATON	2210	C	ALA	117	191.790	106.417	-141.278	1.00	52.98	C23
ATON	2211	C	ALA	117	191.788	106.355	-143.435	1.00	52.98	C23
ATON	2212	C	ALA	117	191.786	106.293	-145.593	1.00	52.98	C23
ATON	2213	C	ALA	117	191.784	106.231	-147.750	1.00	52.98	C23
ATON	2214	C	ALA	117	191.782	106.169	-149.908	1.00	52.98	C23
ATON	2215	C	ALA	117	191.780	106.107	-152.065	1.00	52.98	C23
ATON	2216	C	ALA	117	191.778	106.045	-154.223	1.00	52.98	C23
ATON	2217	C	ALA	117	191.776	105.983	-156.380	1.00	52.98	C23
ATON	2218	C	ALA	117	191.774	105.921	-158.538	1.00	52.98	C23
ATON	2219	C	ALA	117	191.772	105.859	-160.695	1.00	52.98	C23
ATON	2220	C	ALA	117	191.770	105.797	-162.853	1.00	52.98	C23
ATON	2221	C	ALA	117	191.768	105.735	-165.010	1.00	52.98	C23
ATON	2222	C	ALA	117	191.766	105.673	-167.168	1.00	52.98	C23
ATON	2223	C	ALA	117	191.764	105.611	-169.325	1.00	52.98	C23
ATON	2224	C	ALA	117	191.762	105.549	-171.483	1.00	52.98	C23
ATON	2225	C	ALA	117	191.760	105.487	-173.640	1.00	52.98	C23
ATON	2226	C	ALA	117	191.758	105.425	-175.798	1.00	52.98	C23
ATON	2227	C	ALA	117	191.756	105.363	-177.955	1.00	52.98	C23
ATON	2228	C	ALA	117	191.754	105.301	-180.113	1.00	52.98	C23
ATON	2229	C	ALA	117	191.752	105.239	-182.270	1.00	52.98	C23
ATON	2230	C								

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AT00	1023	C	VAL	11	127.529	82.007	-66.009	1.00	41.79	0017
AT00	1024	C	VAL	11	128.140	82.107	-66.109	1.00	41.79	0017
AT00	1025	C	VAL	11	128.693	82.207	-66.209	1.00	41.79	0017
AT00	1026	C	VAL	11	129.246	82.307	-66.309	1.00	41.79	0017
AT00	1027	C	VAL	11	129.799	82.407	-66.409	1.00	41.79	0017
AT00	1028	C	VAL	11	130.352	82.507	-66.509	1.00	41.79	0017
AT00	1029	C	VAL	11	130.905	82.607	-66.609	1.00	41.79	0017
AT00	1030	C	VAL	11	131.458	82.707	-66.709	1.00	41.79	0017
AT00	1031	C	VAL	11	132.011	82.807	-66.809	1.00	41.79	0017
AT00	1032	C	VAL	11	132.564	82.907	-66.909	1.00	41.79	0017
AT00	1033	C	VAL	11	133.117	83.007	-67.009	1.00	41.79	0017
AT00	1034	C	VAL	11	133.670	83.107	-67.109	1.00	41.79	0017
AT00	1035	C	VAL	11	134.223	83.207	-67.209	1.00	41.79	0017
AT00	1036	C	VAL	11	134.776	83.307	-67.309	1.00	41.79	0017
AT00	1037	C	VAL	11	135.329	83.407	-67.409	1.00	41.79	0017
AT00	1038	C	VAL	11	135.882	83.507	-67.509	1.00	41.79	0017
AT00	1039	C	VAL	11	136.435	83.607	-67.609	1.00	41.79	0017
AT00	1040	C	VAL	11	136.988	83.707	-67.709	1.00	41.79	0017
AT00	1041	C	VAL	11	137.541	83.807	-67.809	1.00	41.79	0017
AT00	1042	C	VAL	11	138.094	83.907	-67.909	1.00	41.79	0017
AT00	1043	C	VAL	11	138.647	84.007	-68.009	1.00	41.79	0017
AT00	1044	C	VAL	11	139.200	84.107	-68.109	1.00	41.79	0017
AT00	1045	C	VAL	11	139.753	84.207	-68.209	1.00	41.79	0017
AT00	1046	C	VAL	11	140.306	84.307	-68.309	1.00	41.79	0017
AT00	1047	C	VAL	11	140.859	84.407	-68.409	1.00	41.79	0017
AT00	1048	C	VAL	11	141.412	84.507	-68.509	1.00	41.79	0017
AT00	1049	C	VAL	11	141.965	84.607	-68.609	1.00	41.79	0017
AT00	1050	C	VAL	11	142.518	84.707	-68.709	1.00	41.79	0017
AT00	1051	C	VAL	11	143.071	84.807	-68.809	1.00	41.79	0017
AT00	1052	C	VAL	11	143.624	84.907	-68.909	1.00	41.79	0017
AT00	1053	C	VAL	11	144.177	85.007	-69.009	1.00	41.79	0017
AT00	1054	C	VAL	11	144.730	85.107	-69.109	1.00	41.79	0017
AT00	1055	C	VAL	11	145.283	85.207	-69.209	1.00	41.79	0017
AT00	1056	C	VAL	11	145.836	85.307	-69.309	1.00	41.79	0017
AT00	1057	C	VAL	11	146.389	85.407	-69.409	1.00	41.79	0017
AT00	1058	C	VAL	11	146.942	85.507	-69.509	1.00	41.79	0017
AT00	1059	C	VAL	11	147.495	85.607	-69.609	1.00	41.79	0017
AT00	1060	C	VAL	11	148.048	85.707	-69.709	1.00	41.79	0017
AT00	1061	C	VAL	11	148.601	85.807	-69.809	1.00	41.79	0017
AT00	1062	C	VAL	11	149.154	85.907	-69.909	1.00	41.79	0017
AT00	1063	C	VAL	11	149.707	86.007	-70.009	1.00	41.79	0017
AT00	1064	C	VAL	11	150.260	86.107	-70.109	1.00	41.79	0017
AT00	1065	C	VAL	11	150.813	86.207	-70.209	1.00	41.79	0017
AT00	1066	C	VAL	11	151.366	86.307	-70.309	1.00	41.79	0017
AT00	1067	C	VAL	11	151.919	86.407	-70.409	1.00	41.79	0017
AT00	1068	C	VAL	11	152.472	86.507	-70.509	1.00	41.79	0017
AT00	1069	C	VAL	11	153.025	86.607	-70.609	1.00	41.79	0017
AT00	1070	C	VAL	11	153.578	86.707	-70.709	1.00	41.79	0017
AT00	1071	C	VAL	11	154.131	86.807	-70.809	1.00	41.79	0017
AT00	1072	C	VAL	11	154.684	86.907	-70.909	1.00	41.79	0017
AT00	1073	C	VAL	11	155.237	87.007	-71.009	1.00	41.79	0017
AT00	1074	C	VAL	11	155.790	87.107	-71.109	1.00	41.79	0017
AT00	1075	C	VAL	11	156.343	87.207	-71.209	1.00	41.79	0017
AT00	1076	C	VAL	11	156.896	87.307	-71.309	1.00	41.79	0017
AT00	1077	C	VAL	11	157.449	87.407	-71.409	1.00	41.79	0017
AT00	1078	C	VAL	11	158.002	87.507	-71.509	1.00	41.79	0017
AT00	1079	C	VAL	11	158.555	87.607	-71.609	1.00	41.79	0017
AT00	1080	C	VAL	11	159.108	87.707	-71.709	1.00	41.79	0017
AT00	1081	C	VAL	11	159.661	87.807	-71.809	1.00	41.79	0017
AT00	1082	C	VAL	11	160.214	87.907	-71.909	1.00	41.79	0017
AT00	1083	C	VAL	11	160.767	88.007	-72.009	1.00	41.79	0017
AT00	1084	C	VAL	11	161.320	88.107	-72.109	1.00	41.79	0017
AT00	1085	C	VAL	11	161.873	88.207	-72.209	1.00	41.79	0017
AT00	1086	C	VAL	11	162.426	88.307	-72.309	1.00	41.79	0017
AT00	1087	C	VAL	11	162.979	88.407	-72.409	1.00	41.79	0017
AT00	1088	C	VAL	11	163.532	88.507	-72.509	1.00	41.79	0017
AT00	1089	C	VAL	11	164.085	88.607	-72.609	1.00	41.79	0017
AT00	1090	C	VAL	11	164.638	88.707	-72.709	1.00	41.79	0017
AT00	1091	C	VAL	11	165.191	88.807	-72.809	1.00	41.79	0017
AT00	1092	C	VAL	11	165.744	88.907	-72.909	1.00	41.79	0017
AT00	1093	C	VAL	11	166.297	89.007	-73.009	1.00	41.79	0017
AT00	1094	C	VAL	11	166.850	89.107	-73.109	1.00	41.79	0017
AT00	1095	C	VAL	11	167.403	89.207	-73.209	1.00	41.79	0017
AT00	1096	C	VAL	11	167.956	89.307	-73.309	1.00	41.79	0017
AT00	1097	C	VAL	11	168.509	89.407	-73.409	1.00	41.79	0017
AT00	1098	C	VAL	11	169.062	89.507	-73.509	1.00	41.79	0017
AT00	1099	C	VAL	11	169.615	89.607	-73.609	1.00	41.79	0017
AT00	1100	C	VAL	11	170.168	89.707	-73.709	1.00	41.79	0017
AT00	1101	C	VAL	11	170.721	89.807	-73.809	1.00	41.79	0017
AT00	1102	C	VAL	11	171.274	89.907	-73.909	1.00	41.79	0017
AT00	1103	C	VAL	11	171.827	90.007	-74.009	1.00	41.79	0017
AT00	1104	C	VAL	11	172.380	90.107	-74.109	1.00	41.79	0017
AT00	1105	C	VAL	11	172.933	90.207	-74.209	1.00	41.79	0017
AT00	1106	C	VAL	11	173.486	90.307	-74.309	1.00	41.79	0017
AT00	1107	C	VAL	11	174.039	90.407	-74.409	1.00	41.79	0017
AT00	1108	C	VAL	11	174.592	90.507	-74.509	1.00	41.79	0017
AT00	1109	C	VAL	11	175.145	90.607	-74.609	1.00	41.79	0017
AT00	1110	C	VAL	11	175.698	90.707	-74.709	1.00	41.79	0017
AT00	1111	C	VAL	11	176.251	90.807	-74.809	1.00	41.79	0017
AT00	1112	C	VAL	11	176.804	90.907	-74.909	1.00	41.79	0017
AT00	1113	C	VAL	11	177.357	91.007	-75.009	1.00	41.79	0017
AT00	1114	C	VAL	11	177.910	91.107	-75.109	1.00	41.79	0017
AT00	1115	C	VAL	11	178.463	91.207	-75.209	1.00	41.79	0017
AT00	1116	C	VAL	11	179.016	91.307	-75.309	1.00	41.79	0017
AT00	1117	C	VAL	11	179.569	91.407	-75.409	1.00	41.79	0017
AT00	1118	C	VAL	11	180.122	91.507	-75.509	1.00	41.79	0017
AT00	1119	C	VAL	11	180.675	91.607	-75.609	1.00	41.79	0017
AT00	1120	C	VAL	11	181.228	91.707	-75.709	1.00	41.79	0017
AT00	1121	C	VAL	11	181.781	91.807	-75.809	1.00	41.79	0017
AT00	1122	C	VAL	11	182.334	91.907	-75.909	1.00	41.79	0017
AT00	1123	C	VAL	11	182.887	92.007	-76.009	1.00	41.79	0017
AT00	1124	C	VAL	11	183.440	92.107	-76.109	1.00	41.79	0017
AT00	1125	C	VAL	11	183.993	92.207	-76.209	1.00	41.79	0017
AT00	1126	C	VAL	11	184.546	92.307	-76.309	1.00	41.79	0017
AT00	1127	C	VAL	11	185.099	92.407	-76.409	1.00	41.79	0017
AT00	1128	C	VAL	11	185.652	92.507	-76.509	1.00	41.79	0017
AT00	1129	C	VAL	11	186.205	92.607	-76.609	1.00	41.79	0017
AT00	1130	C	VAL	11	186.758	92.707	-76.709	1.00	41.79	0017
AT00	1131	C	VAL	11	187.311	92.807	-76.809	1.00	41.79	0017
AT00	1132	C	VAL	11	187.864	92.907	-76.909	1.00	41.79	0017
AT00	1133	C	VAL	11	188.417	93.007	-77.009	1.00	41.79	0017
AT00	1134	C	VAL	11	188.970	93.107	-77.109	1.00	41.79	0017
AT00	1135	C	VAL	11	189.523	93.207	-77.209	1.00	41.79	0017
AT00	1136	C	VAL	11	190.076	93.307	-77.309	1.00	41.79	0017
AT00	1137	C	VAL	11	190.629	93.407	-77.409	1.00	41.79	0017
AT00	1138	C	VAL	11	191.182	93.507	-77.509	1.00	41.79	0017
AT00	1139	C	VAL	11	191.735	93.607	-77.609	1.00	41.79	0017
AT00	1140	C	VAL	11	192.288	93.707	-77.709	1.00	41.79	0017
AT00	1141	C	VAL	11	192.841	93.807	-77.809	1.00	41.79	0017
AT00	1142	C	VAL	11	193.394	93.907	-77.909	1.00	41.79	0017
AT00	1143	C	VAL							

EP01	111.011	76.037	-11.152	1.00	76.26	0011	EP01	1274	81.434	63	111.095	69.156	-36.494	1.00	51.00	0017
EP02	111.003	77.964	-12.567	1.00	71.15	0012	EP02	1275	82.153	60	110.823	70.842	-39.799	1.00	51.89	0017
EP03	111.004	77.965	-11.716	1.00	71.15	0013	EP03	1276	82.153	60	111.004	71.011	-39.721	1.00	54.23	0017
EP04	111.005	77.966	-11.700	1.00	71.15	0014	EP04	1277	82.153	60	111.005	71.011	-39.721	1.00	54.23	0017
EP05	111.006	77.967	-11.700	1.00	71.15	0015	EP05	1278	82.153	60	111.006	71.011	-39.721	1.00	54.23	0017
EP06	111.007	77.968	-11.700	1.00	71.15	0016	EP06	1279	82.153	60	111.007	71.011	-39.721	1.00	54.23	0017
EP07	111.008	77.969	-11.700	1.00	71.15	0017	EP07	1280	82.153	60	111.008	71.011	-39.721	1.00	54.23	0017
EP08	111.009	77.970	-11.700	1.00	71.15	0018	EP08	1281	82.153	60	111.009	71.011	-39.721	1.00	54.23	0017
EP09	111.010	77.971	-11.700	1.00	71.15	0019	EP09	1282	82.153	60	111.010	71.011	-39.721	1.00	54.23	0017
EP10	111.011	77.972	-11.700	1.00	71.15	0020	EP10	1283	82.153	60	111.011	71.011	-39.721	1.00	54.23	0017
EP11	111.012	77.973	-11.700	1.00	71.15	0021	EP11	1284	82.153	60	111.012	71.011	-39.721	1.00	54.23	0017
EP12	111.013	77.974	-11.700	1.00	71.15	0022	EP12	1285	82.153	60	111.013	71.011	-39.721	1.00	54.23	0017
EP13	111.014	77.975	-11.700	1.00	71.15	0023	EP13	1286	82.153	60	111.014	71.011	-39.721	1.00	54.23	0017
EP14	111.015	77.976	-11.700	1.00	71.15	0024	EP14	1287	82.153	60	111.015	71.011	-39.721	1.00	54.23	0017
EP15	111.016	77.977	-11.700	1.00	71.15	0025	EP15	1288	82.153	60	111.016	71.011	-39.721	1.00	54.23	0017
EP16	111.017	77.978	-11.700	1.00	71.15	0026	EP16	1289	82.153	60	111.017	71.011	-39.721	1.00	54.23	0017
EP17	111.018	77.979	-11.700	1.00	71.15	0027	EP17	1290	82.153	60	111.018	71.011	-39.721	1.00	54.23	0017
EP18	111.019	77.980	-11.700	1.00	71.15	0028	EP18	1291	82.153	60	111.019	71.011	-39.721	1.00	54.23	0017
EP19	111.020	77.981	-11.700	1.00	71.15	0029	EP19	1292	82.153	60	111.020	71.011	-39.721	1.00	54.23	0017
EP20	111.021	77.982	-11.700	1.00	71.15	0030	EP20	1293	82.153	60	111.021	71.011	-39.721	1.00	54.23	0017
EP21	111.022	77.983	-11.700	1.00	71.15	0031	EP21	1294	82.153	60	111.022	71.011	-39.721	1.00	54.23	0017
EP22	111.023	77.984	-11.700	1.00	71.15	0032	EP22	1295	82.153	60	111.023	71.011	-39.721	1.00	54.23	0017
EP23	111.024	77.985	-11.700	1.00	71.15	0033	EP23	1296	82.153	60	111.024	71.011	-39.721	1.00	54.23	0017
EP24	111.025	77.986	-11.700	1.00	71.15	0034	EP24	1297	82.153	60	111.025	71.011	-39.721	1.00	54.23	0017
EP25	111.026	77.987	-11.700	1.00	71.15	0035	EP25	1298	82.153	60	111.026	71.011	-39.721	1.00	54.23	0017
EP26	111.027	77.988	-11.700	1.00	71.15	0036	EP26	1299	82.153	60	111.027	71.011	-39.721	1.00	54.23	0017
EP27	111.028	77.989	-11.700	1.00	71.15	0037	EP27	1300	82.153	60	111.028	71.011	-39.721	1.00	54.23	0017
EP28	111.029	77.990	-11.700	1.00	71.15	0038	EP28	1301	82.153	60	111.029	71.011	-39.721	1.00	54.23	0017
EP29	111.030	77.991	-11.700	1.00	71.15	0039	EP29	1302	82.153	60	111.030	71.011	-39.721	1.00	54.23	0017
EP30	111.031	77.992	-11.700	1.00	71.15	0040	EP30	1303	82.153	60	111.031	71.011	-39.721	1.00	54.23	0017
EP31	111.032	77.993	-11.700	1.00	71.15	0041	EP31	1304	82.153	60	111.032	71.011	-39.721	1.00	54.23	0017
EP32	111.033	77.994	-11.700	1.00	71.15	0042	EP32	1305	82.153	60	111.033	71.011	-39.721	1.00	54.23	0017
EP33	111.034	77.995	-11.700	1.00	71.15	0043	EP33	1306	82.153	60	111.034	71.011	-39.721	1.00	54.23	0017
EP34	111.035	77.996	-11.700	1.00	71.15	0044	EP34	1307	82.153	60	111.035	71.011	-39.721	1.00	54.23	0017
EP35	111.036	77.997	-11.700	1.00	71.15	0045	EP35	1308	82.153	60	111.036	71.011	-39.721	1.00	54.23	0017
EP36	111.037	77.998	-11.700	1.00	71.15	0046	EP36	1309	82.153	60	111.037	71.011	-39.721	1.00	54.23	0017
EP37	111.038	77.999	-11.700	1.00	71.15	0047	EP37	1310	82.153	60	111.038	71.011	-39.721	1.00	54.23	0017
EP38	111.039	78.000	-11.700	1.00	71.15	0048	EP38	1311	82.153	60	111.039	71.011	-39.721	1.00	54.23	0017
EP39	111.040	78.001	-11.700	1.00	71.15	0049	EP39	1312	82.153	60	111.040	71.011	-39.721	1.00	54.23	0017
EP40	111.041	78.002	-11.700	1.00	71.15	0050	EP40	1313	82.153	60	111.041	71.011	-39.721	1.00	54.23	0017
EP41	111.042	78.003	-11.700	1.00	71.15	0051	EP41	1314	82.153	60	111.042	71.011	-39.721	1.00	54.23	0017
EP42	111.043	78.004	-11.700	1.00	71.15	0052	EP42	1315	82.153	60	111.043	71.011	-39.721	1.00	54.23	0017
EP43	111.044	78.005	-11.700	1.00	71.15	0053	EP43	1316	82.153	60	111.044	71.011	-39.721	1.00	54.23	0017
EP44	111.045	78.006	-11.700	1.00	71.15	0054	EP44	1317	82.153	60	111.045	71.011	-39.721	1.00	54.23	0017
EP45	111.046	78.007	-11.700	1.00	71.15	0055	EP45	1318	82.153	60	111.046	71.011	-39.721	1.00	54.23	0017
EP46	111.047	78.008	-11.700	1.00	71.15	0056	EP46	1319	82.153	60	111.047	71.011	-39.721	1.00	54.23	0017
EP47	111.048	78.009	-11.700	1.00	71.15	0057	EP47	1320	82.153	60	111.048	71.011	-39.721	1.00	54.23	0017
EP48	111.049	78.010	-11.700	1.00	71.15	0058	EP48	1321	82.153	60	111.049	71.011	-39.721	1.00	54.23	0017
EP49	111.050	78.011	-11.700	1.00	71.15	0059	EP49	1322	82.153	60	111.050	71.011	-39.721	1.00	54.23	0017
EP50	111.051	78.012	-11.700	1.00	71.15	0060	EP50	1323	82.153	60	111.051	71.011	-39.721	1.00	54.23	0017
EP51	111.052	78.013	-11.700	1.00	71.15	0061	EP51	1324	82.153	60	111.052	71.011	-39.721	1.00	54.23	0017
EP52	111.053	78.014	-11.700	1.00	71.15	0062	EP52	1325	82.153	60	111.053	71.011	-39.721	1.00	54.23	0017
EP53	111.054	78.015	-11.700	1.00	71.15	0063	EP53	1326	82.153	60	111.054	71.011	-39.721	1.00	54.23	0017
EP54	111.055	78.016	-11.700	1.00	71.15	0064	EP54	1327	82.153	60	111.055	71.011	-39.721	1.00	54.23	0017
EP55	111.056	78.017	-11.700	1.00	71.15	0065	EP55	1328	82.153	60	111.056	71.011	-39.721	1.00	54.23	0017
EP56	111.057	78.018	-11.700	1.00	71.15	0066	EP56	1329	82.153	60	111.057	71.011	-39.721	1.00	54.23	0017
EP57	111.058	78.019	-11.700	1.00	71.15	0067	EP57	1330	82.153	60	111.058	71.011	-39.721	1.00	54.23	0017
EP58	111.059	78.020	-11.700	1.00	71.15	0068	EP58	1331	82.153	60	111.059	71.011	-39.721	1.00	54.23	0017
EP59	111.060	78.021	-11.700	1.00	71.15	0069	EP59	1332	82.153	60	111.060	71.011	-39.721	1.00	54.23	0017
EP60	111.061	78.022	-11.700	1.00	71.15	0070	EP60	1333	82.153	60	111.061	71.011	-39.721	1.00	54.23	0017
EP61	111.062	78.023	-11.700	1.00	71.15	0071	EP61	1334	82.153	60	111.062	71.011	-39.721	1.00	54.23	0017
EP62	111.063	78.024	-11.700	1.00	71.15	0072	EP62	1335	82.153	60	111.063	71.011	-39.721	1.00	54.23	0017
EP63	111.064	78.025	-11.700	1.00	71.15	0073	EP63	1336	82.153	60	111.064	71.011	-39.721	1.00	54.23	0017
EP64	111.065	78.026	-11.700	1.00	71.15	0074	EP64	1337	82.153	60	111.065	71.011	-39.721	1.00	54.23	0017
EP65	111.066	78.027	-11.700	1.00	71.15	0075	EP65	1338	82.153	60	111.066	71.011	-39.721	1.00	54.23	0017
EP66	111.067	78.028	-11.700	1.00	71.15	0076	EP66	1339	82.153	60	111.067	71.011	-39.721	1.00	54.23	0017
EP67	111.068	78.029	-11.700	1.00	71.15	0077	EP67	1340	82.153	60	111.068	71.011	-39.721	1.00	54.23	0017
EP68	111.069	78.030	-11.700	1.00	71.15	0078	EP68	1341	82.153	60	111.069	71.011	-39.721	1.00	54.23	0017
EP69	111.070	78.031	-11.700	1.00	71.15	0079	EP69	1342	82.153	60	111.070	71.011	-39.721	1.00	54.23	0017
EP70	111.071	78.032	-11.700	1.00	71.15	0080	EP70	1343	82.153	60	111.071	71.011	-39.721	1.00	54.23	0017
EP71	111.072	78.033	-11.700	1.00	71.15	0081	EP71	1344	82.153	60	111.072	71.011	-39.721	1.00	54.23	0017
EP72	111.073	78.034	-11.700	1.00	71.15											



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EP01	1969	C	CLP	62	196.999	134.374	-66.623	1.00	82.41	8210
EP01	1970	CH	CLP	62	197.274	134.546	-62.275	1.00	82.41	8210
EP01	1971	CH	CLP	62	197.549	134.719	-62.170	1.00	82.41	8210
EP01	1972	C	CLP	62	197.824	134.892	-62.071	1.00	82.41	8210
EP01	1973	C	CLP	62	198.100	135.065	-61.972	1.00	82.41	8210
EP01	1974	C	CLP	62	198.375	135.238	-61.873	1.00	82.41	8210
EP01	1975	C	CLP	62	198.650	135.411	-61.774	1.00	82.41	8210
EP01	1976	C	CLP	62	198.925	135.584	-61.675	1.00	82.41	8210
EP01	1977	C	CLP	62	199.200	135.757	-61.576	1.00	82.41	8210
EP01	1978	C	CLP	62	199.475	135.930	-61.477	1.00	82.41	8210
EP01	1979	C	CLP	62	199.750	136.103	-61.378	1.00	82.41	8210
EP01	1980	C	CLP	62	200.025	136.276	-61.279	1.00	82.41	8210
EP01	1981	C	CLP	62	200.300	136.449	-61.180	1.00	82.41	8210
EP01	1982	C	CLP	62	200.575	136.622	-61.081	1.00	82.41	8210
EP01	1983	C	CLP	62	200.850	136.795	-60.982	1.00	82.41	8210
EP01	1984	C	CLP	62	201.125	136.968	-60.883	1.00	82.41	8210
EP01	1985	C	CLP	62	201.400	137.141	-60.784	1.00	82.41	8210
EP01	1986	C	CLP	62	201.675	137.314	-60.685	1.00	82.41	8210
EP01	1987	C	CLP	62	201.950	137.487	-60.586	1.00	82.41	8210
EP01	1988	C	CLP	62	202.225	137.660	-60.487	1.00	82.41	8210
EP01	1989	C	CLP	62	202.500	137.833	-60.388	1.00	82.41	8210
EP01	1990	C	CLP	62	202.775	138.006	-60.289	1.00	82.41	8210
EP01	1991	C	CLP	62	203.050	138.179	-60.190	1.00	82.41	8210
EP01	1992	C	CLP	62	203.325	138.352	-60.091	1.00	82.41	8210
EP01	1993	C	CLP	62	203.600	138.525	-59.992	1.00	82.41	8210
EP01	1994	C	CLP	62	203.875	138.698	-59.893	1.00	82.41	8210
EP01	1995	C	CLP	62	204.150	138.871	-59.794	1.00	82.41	8210
EP01	1996	C	CLP	62	204.425	139.044	-59.695	1.00	82.41	8210
EP01	1997	C	CLP	62	204.700	139.217	-59.596	1.00	82.41	8210
EP01	1998	C	CLP	62	204.975	139.390	-59.497	1.00	82.41	8210
EP01	1999	C	CLP	62	205.250	139.563	-59.398	1.00	82.41	8210
EP01	2000	C	CLP	62	205.525	139.736	-59.299	1.00	82.41	8210
EP01	2001	C	CLP	62	205.800	139.909	-59.200	1.00	82.41	8210
EP01	2002	C	CLP	62	206.075	140.082	-59.101	1.00	82.41	8210
EP01	2003	C	CLP	62	206.350	140.255	-59.002	1.00	82.41	8210
EP01	2004	C	CLP	62	206.625	140.428	-58.903	1.00	82.41	8210
EP01	2005	C	CLP	62	206.900	140.601	-58.804	1.00	82.41	8210
EP01	2006	C	CLP	62	207.175	140.774	-58.705	1.00	82.41	8210
EP01	2007	C	CLP	62	207.450	140.947	-58.606	1.00	82.41	8210
EP01	2008	C	CLP	62	207.725	141.120	-58.507	1.00	82.41	8210
EP01	2009	C	CLP	62	208.000	141.293	-58.408	1.00	82.41	8210
EP01	2010	C	CLP	62	208.275	141.466	-58.309	1.00	82.41	8210
EP01	2011	C	CLP	62	208.550	141.639	-58.210	1.00	82.41	8210
EP01	2012	C	CLP	62	208.825	141.812	-58.111	1.00	82.41	8210
EP01	2013	C	CLP	62	209.100	141.985	-58.012	1.00	82.41	8210
EP01	2014	C	CLP	62	209.375	142.158	-57.913	1.00	82.41	8210
EP01	2015	C	CLP	62	209.650	142.331	-57.814	1.00	82.41	8210
EP01	2016	C	CLP	62	209.925	142.504	-57.715	1.00	82.41	8210
EP01	2017	C	CLP	62	210.200	142.677	-57.616	1.00	82.41	8210
EP01	2018	C	CLP	62	210.475	142.850	-57.517	1.00	82.41	8210
EP01	2019	C	CLP	62	210.750	143.023	-57.418	1.00	82.41	8210
EP01	2020	C	CLP	62	211.025	143.196	-57.319	1.00	82.41	8210
EP01	2021	C	CLP	62	211.300	143.369	-57.220	1.00	82.41	8210
EP01	2022	C	CLP	62	211.575	143.542	-57.121	1.00	82.41	8210
EP01	2023	C	CLP	62	211.850	143.715	-57.022	1.00	82.41	8210
EP01	2024	C	CLP	62	212.125	143.888	-56.923	1.00	82.41	8210
EP01	2025	C	CLP	62	212.400	144.061	-56.824	1.00	82.41	8210
EP01	2026	C	CLP	62	212.675	144.234	-56.725	1.00	82.41	8210
EP01	2027	C	CLP	62	212.950	144.407	-56.626	1.00	82.41	8210
EP01	2028	C	CLP	62	213.225	144.580	-56.527	1.00	82.41	8210
EP01	2029	C	CLP	62	213.500	144.753	-56.428	1.00	82.41	8210
EP01	2030	C	CLP	62	213.775	144.926	-56.329	1.00	82.41	8210
EP01	2031	C	CLP	62	214.050	145.099	-56.230	1.00	82.41	8210
EP01	2032	C	CLP	62	214.325	145.272	-56.131	1.00	82.41	8210
EP01	2033	C	CLP	62	214.600	145.445	-56.032	1.00	82.41	8210
EP01	2034	C	CLP	62	214.875	145.618	-55.933	1.00	82.41	8210
EP01	2035	C	CLP	62	215.150	145.791	-55.834	1.00	82.41	8210
EP01	2036	C	CLP	62	215.425	145.964	-55.735	1.00	82.41	8210
EP01	2037	C	CLP	62	215.700	146.137	-55.636	1.00	82.41	8210
EP01	2038	C	CLP	62	215.975	146.310	-55.537	1.00	82.41	8210
EP01	2039	C	CLP	62	216.250	146.483	-55.438	1.00	82.41	8210
EP01	2040	C	CLP	62	216.525	146.656	-55.339	1.00	82.41	8210
EP01	2041	C	CLP	62	216.800	146.829	-55.240	1.00	82.41	8210
EP01	2042	C	CLP	62	217.075	147.002	-55.141	1.00	82.41	8210
EP01	2043	C	CLP	62	217.350	147.175	-55.042	1.00	82.41	8210
EP01	2044	C	CLP	62	217.625	147.348	-54.943	1.00	82.41	8210
EP01	2045	C	CLP	62	217.900	147.521	-54.844	1.00	82.41	8210
EP01	2046	C	CLP	62	218.175	147.694	-54.745	1.00	82.41	8210
EP01	2047	C	CLP	62	218.450	147.867	-54.646	1.00	82.41	8210
EP01	2048	C	CLP	62	218.725	148.040	-54.547	1.00	82.41	8210
EP01	2049	C	CLP	62	219.000	148.213	-54.448	1.00	82.41	8210
EP01	2050	C	CLP	62	219.275	148.386	-54.349	1.00	82.41	8210
EP01	2051	C	CLP	62	219.550	148.559	-54.250	1.00	82.41	8210
EP01	2052	C	CLP	62	219.825	148.732	-54.151	1.00	82.41	8210
EP01	2053	C	CLP	62	220.100	148.905	-54.052	1.00	82.41	8210
EP01	2054	C	CLP	62	220.375	149.078	-53.953	1.00	82.41	8210
EP01	2055	C	CLP	62	220.650	149.251	-53.854	1.00	82.41	8210
EP01	2056	C	CLP	62	220.925	149.424	-53.755	1.00	82.41	8210
EP01	2057	C	CLP	62	221.200	149.597	-53.656	1.00	82.41	8210
EP01	2058	C	CLP	62	221.475	149.770	-53.557	1.00	82.41	8210
EP01	2059	C	CLP	62	221.750	149.943	-53.458	1.00	82.41	8210
EP01	2060	C	CLP	62	222.025	150.116	-53.359	1.00	82.41	8210
EP01	2061	C	CLP	62	222.300	150.289	-53.260	1.00	82.41	8210
EP01	2062	C	CLP	62	222.575	150.462	-53.161	1.00	82.41	8210
EP01	2063	C	CLP	62	222.850	150.635	-53.062	1.00	82.41	8210
EP01	2064	C	CLP	62	223.125	150.808	-52.963	1.00	82.41	8210
EP01	2065	C	CLP	62	223.400	150.981	-52.864	1.00	82.41	8210
EP01	2066	C	CLP	62	223.675	151.154	-52.765	1.00	82.41	8210
EP01	2067	C	CLP	62	223.950	151.327	-52.666	1.00	82.41	8210
EP01	2068	C	CLP	62	224.225	151.500	-52.567	1.00	82.41	8210
EP01	2069	C	CLP	62	224.500	151.673	-52.468	1.00	82.41	8210
EP01	2070	C	CLP	62	224.775	151.846	-52.369	1.00	82.41	8210
EP01	2071	C	CLP	62	225.050	152.019	-52.270	1.00	82.41	8210
EP01	2072	C	CLP	62	225.325	152.192	-52.171	1.00	82.41	8210
EP01	2073	C	CLP	62	225.600	152.365	-52.072	1.00	82.41	8210
EP01	2074	C	CLP	62	225.875	152.538	-51.973	1.00	82.41	8210
EP01	2075	C	CLP	62	226.150	152.711	-51.874	1.00	82.41	8210
EP01	2076	C	CLP	62	226.425	152.884	-51.775	1.00	82.41	8210
EP01	2077	C	CLP	62	226.700	153.057	-51.676	1.00	82.41	8210
EP01	2078	C	CLP	62	226.975	153.230	-51.577	1.00	82.41	8210
EP01	2079	C	CLP	62	227.250	153.403	-51.478	1.00	82.41	8210
EP01	2080	C	CLP	62	227.525	153.576	-51.379	1.00	82.41	8210
EP01	2081	C	CLP	62	227.800	153.749	-51.280	1.00	82.41	8210
EP01	2082	C	CLP	62	228.075	153.922	-51.181	1.00	82.41	8210
EP01	2083	C	CLP	62	228.350	154.095	-51.082	1.00	82.41	8210
EP01	2084	C	CLP	62	228.625	154.268	-50.983	1.00	82.41	8210
EP01	2085	C	CLP	62	228.900	154.441	-50.884	1.00	82.41	8210
EP01	2086	C	CLP	62	229.175	154.614	-50.785	1.00	82.41	8210

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AT00	0027	CA	100	711.440	91.263	3.897	1.00119.83	3219	AT00	0710	0	100	241.344	140.740	-4.753	1.000.01.30	1729
AT00	0028	CA	100	712.701	92.251	3.898	1.00119.83	3220	AT00	0711	0	100	241.344	140.740	-4.753	1.000.01.30	1730
AT00	0029	CA	100	713.736	93.239	3.899	1.00119.83	3221	AT00	0712	0	100	241.344	140.740	-4.753	1.000.01.30	1731
AT00	0030	CA	100	714.771	94.227	3.900	1.00119.83	3222	AT00	0713	0	100	241.344	140.740	-4.753	1.000.01.30	1732
AT00	0031	CA	100	715.806	95.215	3.901	1.00119.83	3223	AT00	0714	0	100	241.344	140.740	-4.753	1.000.01.30	1733
AT00	0032	CA	100	716.841	96.203	3.902	1.00119.83	3224	AT00	0715	0	100	241.344	140.740	-4.753	1.000.01.30	1734
AT00	0033	CA	100	717.876	97.191	3.903	1.00119.83	3225	AT00	0716	0	100	241.344	140.740	-4.753	1.000.01.30	1735
AT00	0034	CA	100	718.911	98.179	3.904	1.00119.83	3226	AT00	0717	0	100	241.344	140.740	-4.753	1.000.01.30	1736
AT00	0035	CA	100	719.946	99.167	3.905	1.00119.83	3227	AT00	0718	0	100	241.344	140.740	-4.753	1.000.01.30	1737
AT00	0036	CA	100	720.981	100.155	3.906	1.00119.83	3228	AT00	0719	0	100	241.344	140.740	-4.753	1.000.01.30	1738
AT00	0037	CA	100	722.016	101.143	3.907	1.00119.83	3229	AT00	0720	0	100	241.344	140.740	-4.753	1.000.01.30	1739
AT00	0038	CA	100	723.051	102.131	3.908	1.00119.83	3230	AT00	0721	0	100	241.344	140.740	-4.753	1.000.01.30	1740
AT00	0039	CA	100	724.086	103.119	3.909	1.00119.83	3231	AT00	0722	0	100	241.344	140.740	-4.753	1.000.01.30	1741
AT00	0040	CA	100	725.121	104.107	3.910	1.00119.83	3232	AT00	0723	0	100	241.344	140.740	-4.753	1.000.01.30	1742
AT00	0041	CA	100	726.156	105.095	3.911	1.00119.83	3233	AT00	0724	0	100	241.344	140.740	-4.753	1.000.01.30	1743
AT00	0042	CA	100	727.191	106.083	3.912	1.00119.83	3234	AT00	0725	0	100	241.344	140.740	-4.753	1.000.01.30	1744
AT00	0043	CA	100	728.226	107.071	3.913	1.00119.83	3235	AT00	0726	0	100	241.344	140.740	-4.753	1.000.01.30	1745
AT00	0044	CA	100	729.261	108.059	3.914	1.00119.83	3236	AT00	0727	0	100	241.344	140.740	-4.753	1.000.01.30	1746
AT00	0045	CA	100	730.296	109.047	3.915	1.00119.83	3237	AT00	0728	0	100	241.344	140.740	-4.753	1.000.01.30	1747
AT00	0046	CA	100	731.331	110.035	3.916	1.00119.83	3238	AT00	0729	0	100	241.344	140.740	-4.753	1.000.01.30	1748
AT00	0047	CA	100	732.366	111.023	3.917	1.00119.83	3239	AT00	0730	0	100	241.344	140.740	-4.753	1.000.01.30	1749
AT00	0048	CA	100	733.401	112.011	3.918	1.00119.83	3240	AT00	0731	0	100	241.344	140.740	-4.753	1.000.01.30	1750
AT00	0049	CA	100	734.436	113.000	3.919	1.00119.83	3241	AT00	0732	0	100	241.344	140.740	-4.753	1.000.01.30	1751
AT00	0050	CA	100	735.471	114.000	3.920	1.00119.83	3242	AT00	0733	0	100	241.344	140.740	-4.753	1.000.01.30	1752
AT00	0051	CA	100	736.506	115.000	3.921	1.00119.83	3243	AT00	0734	0	100	241.344	140.740	-4.753	1.000.01.30	1753
AT00	0052	CA	100	737.541	116.000	3.922	1.00119.83	3244	AT00	0735	0	100	241.344	140.740	-4.753	1.000.01.30	1754
AT00	0053	CA	100	738.576	117.000	3.923	1.00119.83	3245	AT00	0736	0	100	241.344	140.740	-4.753	1.000.01.30	1755
AT00	0054	CA	100	739.611	118.000	3.924	1.00119.83	3246	AT00	0737	0	100	241.344	140.740	-4.753	1.000.01.30	1756
AT00	0055	CA	100	740.646	119.000	3.925	1.00119.83	3247	AT00	0738	0	100	241.344	140.740	-4.753	1.000.01.30	1757
AT00	0056	CA	100	741.681	120.000	3.926	1.00119.83	3248	AT00	0739	0	100	241.344	140.740	-4.753	1.000.01.30	1758
AT00	0057	CA	100	742.716	121.000	3.927	1.00119.83	3249	AT00	0740	0	100	241.344	140.740	-4.753	1.000.01.30	1759
AT00	0058	CA	100	743.751	122.000	3.928	1.00119.83	3250	AT00	0741	0	100	241.344	140.740	-4.753	1.000.01.30	1760
AT00	0059	CA	100	744.786	123.000	3.929	1.00119.83	3251	AT00	0742	0	100	241.344	140.740	-4.753	1.000.01.30	1761
AT00	0060	CA	100	745.821	124.000	3.930	1.00119.83	3252	AT00	0743	0	100	241.344	140.740	-4.753	1.000.01.30	1762
AT00	0061	CA	100	746.856	125.000	3.931	1.00119.83	3253	AT00	0744	0	100	241.344	140.740	-4.753	1.000.01.30	1763
AT00	0062	CA	100	747.891	126.000	3.932	1.00119.83	3254	AT00	0745	0	100	241.344	140.740	-4.753	1.000.01.30	1764
AT00	0063	CA	100	748.926	127.000	3.933	1.00119.83	3255	AT00	0746	0	100	241.344	140.740	-4.753	1.000.01.30	1765
AT00	0064	CA	100	749.961	128.000	3.934	1.00119.83	3256	AT00	0747	0	100	241.344	140.740	-4.753	1.000.01.30	1766
AT00	0065	CA	100	750.996	129.000	3.935	1.00119.83	3257	AT00	0748	0	100	241.344	140.740	-4.753	1.000.01.30	1767
AT00	0066	CA	100	752.031	130.000	3.936	1.00119.83	3258	AT00	0749	0	100	241.344	140.740	-4.753	1.000.01.30	1768
AT00	0067	CA	100	753.066	131.000	3.937	1.00119.83	3259	AT00	0750	0	100	241.344	140.740	-4.753	1.000.01.30	1769
AT00	0068	CA	100	754.101	132.000	3.938	1.00119.83	3260	AT00	0751	0	100	241.344	140.740	-4.753	1.000.01.30	1770
AT00	0069	CA	100	755.136	133.000	3.939	1.00119.83	3261	AT00	0752	0	100	241.344	140.740	-4.753	1.000.01.30	1771
AT00	0070	CA	100	756.171	134.000	3.940	1.00119.83	3262	AT00	0753	0	100	241.344	140.740	-4.753	1.000.01.30	1772
AT00	0071	CA	100	757.206	135.000	3.941	1.00119.83	3263	AT00	0754	0	100	241.344	140.740	-4.753	1.000.01.30	1773
AT00	0072	CA	100	758.241	136.000	3.942	1.00119.83	3264	AT00	0755	0	100	241.344	140.740	-4.753	1.000.01.30	1774
AT00	0073	CA	100	759.276	137.000	3.943	1.00119.83	3265	AT00	0756	0	100	241.344	140.740	-4.753	1.000.01.30	1775
AT00	0074	CA	100	760.311	138.000	3.944	1.00119.83	3266	AT00	0757	0	100	241.344	140.740	-4.753	1.000.01.30	1776
AT00	0075	CA	100	761.346	139.000	3.945	1.00119.83	3267	AT00	0758	0	100	241.344	140.740	-4.753	1.000.01.30	1777
AT00	0076	CA	100	762.381	140.000	3.946	1.00119.83	3268	AT00	0759	0	100	241.344	140.740	-4.753	1.000.01.30	1778
AT00	0077	CA	100	763.416	141.000	3.947	1.00119.83	3269	AT00	0760	0	100	241.344	140.740	-4.753	1.000.01.30	1779
AT00	0078	CA	100	764.451	142.000	3.948	1.00119.83	3270	AT00	0761	0	100	241.344	140.740	-4.753	1.000.01.30	1780
AT00	0079	CA	100	765.486	143.000	3.949	1.00119.83	3271	AT00	0762	0	100	241.344	140.740	-4.753	1.000.01.30	1781
AT00	0080	CA	100	766.521	144.000	3.950	1.00119.83	3272	AT00	0763	0	100	241.344	140.740	-4.753	1.000.01.30	1782
AT00	0081	CA	100	767.556	145.000	3.951	1.00119.83	3273	AT00	0764	0	100	241.344	140.740	-4.753	1.000.01.30	1783
AT00	0082	CA	100	768.591	146.000	3.952	1.00119.83	3274	AT00	0765	0	100	241.344	140.740	-4.753	1.000.01.30	1784
AT00	0083	CA	100	769.626	147.000	3.953	1.00119.83	3275	AT00	0766	0	100	241.344	140.740	-4.753	1.000.01.30	1785
AT00	0084	CA	100	770.661	148.000	3.954	1.00119.83	3276	AT00	0767	0	100	241.344	140.740	-4.753	1.000.01.30	1786
AT00	0085	CA	100	771.696	149.000	3.955	1.00119.83	3277	AT00	0768	0	100	241.344	140.740	-4.753	1.000.01.30	1787
AT00	0086	CA	100	772.731	150.000	3.956	1.00119.83	3278	AT00	0769	0	100	241.344	140.740	-4.753	1.000.01.30	1788
AT00	0087	CA	100	773.766	151.000	3.957	1.00119.83	3279	AT00	0770	0	100	241.344	140.740	-4.753	1.000.01.30	1789
AT00	0088	CA	100	774.801	152.000	3.958	1.00119.83	3280	AT00	0771	0	100	241.344	140.740	-4.753	1.000.01.30	1790
AT00	0089	CA	100	775.836	153.000	3.959	1.00119.83	3281	AT00	0772	0	100	241.344	140.740	-4.753	1.000.01.30	1791
AT00	0090	CA	100	776.871	154.000	3.960	1.00119.83	3282	AT00	0773	0	100	241.344	140.740	-4.753	1.000.01.30	1792
AT00	0091	CA	100	777.906	155.000	3.961	1.00119.83	3283	AT00	0774	0	100	241.344	140.740	-4.753	1.000.01.30	1793
AT00	0092	CA	100	778.941	156.000	3.962	1.00119.83	3284	AT00	0775	0	100	241.344	140.740	-4.753	1.000.01.30	1794
AT00	0093	CA	100	779.976	157.000	3.963	1.00119.83	3285	AT00	0776	0	100	241.344	14			

AT00	7113	08	YPO	35	248.345	154.244	-0.325	1.00	95.44	113
AT00	7114	08	YPO	35	248.374	153.993	-1.203	1.00	95.44	113
AT00	7115	08	YPO	35	247.962	155.277	-0.492	1.00	95.44	113
AT00	7116	08	YPO	35	247.910	156.222	-0.478	1.00	95.44	113
AT00	7117	08	YPO	35	246.182	155.617	-0.907	1.00	95.44	113
AT00	7118	08	YPO	35	246.323	158.349	-0.776	1.00	95.44	113
AT00	7119	08	YPO	35	245.940	156.343	-1.100	1.00	95.44	113
AT00	7120	08	YPO	35	245.067	156.976	-0.999	1.00	95.44	113
AT00	7121	08	YPO	35	245.714	152.829	-0.470	1.00	95.44	113
AT00	7122	08	YPO	35	245.343	155.251	-0.126	1.00	95.44	113
AT00	7123	08	YPO	35	245.066	156.064	-0.126	1.00	95.44	113
AT00	7124	08	YPO	35	247.254	155.181	-0.902	1.00	95.44	113
AT00	7125	08	YPO	35	246.793	155.754	-0.587	1.00	95.44	113
AT00	7126	08	YPO	35	246.185	156.879	-0.163	1.00	95.44	113
AT00	7127	08	YPO	35	246.373	155.156	-0.990	1.00	95.44	113
AT00	7128	08	YPO	35	245.824	157.017	-0.721	1.00	95.44	113
AT00	7129	08	YPO	35	245.384	156.187	-0.393	1.00	95.44	113
AT00	7130	08	YPO	35	244.832	156.873	-0.730	1.00	95.44	113
AT00	7131	08	YPO	35	246.073	153.923	-0.920	1.00	95.44	113
AT00	7132	08	YPO	35	245.704	153.953	-0.124	1.00	95.44	113
AT00	7133	08	YPO	35	242.160	153.474	-0.415	1.00	95.44	113
AT00	7134	08	YPO	35	242.275	152.943	-0.913	1.00	95.44	113
AT00	7135	08	YPO	35	242.113	152.836	-0.163	1.00	95.44	113
AT00	7136	08	YPO	35	244.847	152.895	-0.441	1.00	95.44	113
AT00	7137	08	YPO	35	245.915	152.618	-0.174	1.00	95.44	113
AT00	7138	08	YPO	35	244.144	152.846	-0.102	1.00	95.44	113
AT00	7139	08	YPO	35	244.041	151.340	-0.920	1.00	95.44	113
AT00	7140	08	YPO	35	243.274	151.509	-0.364	1.00	95.44	113
AT00	7141	08	YPO	35	243.197	154.040	-0.461	1.00	95.44	113
AT00	7142	08	YPO	35	243.723	151.377	-0.666	1.00	95.44	113
AT00	7143	08	YPO	35	243.123	150.251	-0.128	1.00	95.44	113
AT00	7144	08	YPO	35	243.064	149.423	-0.101	1.00	95.44	113
AT00	7145	08	YPO	35	240.524	149.836	-0.179	1.00	95.44	113
AT00	7146	08	YPO	35	240.187	150.702	-0.113	1.00	95.44	113
AT00	7147	08	YPO	35	242.687	150.531	-0.154	1.00	95.44	113
AT00	7148	08	YPO	35	245.961	153.143	-0.423	1.00	95.44	113
AT00	7149	08	YPO	35	247.244	150.490	-0.620	1.00	95.44	113
AT00	7150	08	YPO	35	246.444	151.113	-0.610	1.00	95.44	113
AT00	7151	08	YPO	35	247.113	149.100	-0.415	1.00	95.44	113
AT00	7152	08	YPO	35	247.157	150.172	-0.143	1.00	95.44	113
AT00	7153	08	YPO	35	246.324	152.120	-0.101	1.00	95.44	113
AT00	7154	08	YPO	35	247.073	150.267	-0.197	1.00	95.44	113
AT00	7155	08	YPO	35	246.325	150.916	-0.149	1.00	95.44	113
AT00	7156	08	YPO	35	245.440	149.349	-0.157	1.00	95.44	113
AT00	7157	08	YPO	35	246.114	150.830	-0.116	1.00	95.44	113
AT00	7158	08	YPO	35	247.188	149.527	-0.170	1.00	95.44	113
AT00	7159	08	YPO	35	245.704	151.464	-0.101	1.00	95.44	113
AT00	7160	08	YPO	35	244.900	150.176	-0.423	1.00	95.44	113
AT00	7161	08	YPO	35	245.040	151.000	-0.100	1.00	95.44	113
AT00	7162	08	YPO	35	245.440	152.175	-0.170	1.00	95.44	113
AT00	7163	08	YPO	35	247.295	151.009	-0.100	1.00	95.44	113
AT00	7164	08	YPO	35	247.243	151.000	-0.100	1.00	95.44	113
AT00	7165	08	YPO	35	247.790	152.012	-0.143	1.00	95.44	113
AT00	7166	08	YPO	35	246.715	151.245	-0.143	1.00	95.44	113
AT00	7167	08	YPO	35	246.361	151.000	-0.100	1.00	95.44	113
AT00	7168	08	YPO	35	246.961	152.000	-0.100	1.00	95.44	113
AT00	7169	08	YPO	35	246.715	151.000	-0.100	1.00	95.44	113
AT00	7170	08	YPO	35	247.145	152.000	-0.100	1.00	95.44	113
AT00	7171	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7172	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7173	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7174	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7175	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7176	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7177	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7178	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7179	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7180	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7181	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7182	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7183	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7184	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7185	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7186	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7187	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7188	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7189	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7190	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7191	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7192	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7193	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7194	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7195	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7196	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7197	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7198	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7199	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7200	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7201	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7202	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7203	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7204	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7205	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7206	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7207	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7208	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7209	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7210	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7211	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7212	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7213	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7214	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7215	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7216	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7217	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7218	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7219	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7220	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7221	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7222	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7223	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7224	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7225	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7226	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7227	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7228	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7229	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113
AT00	7230	08	YPO	35	246.127	154.000	-0.100	1.00	95.44	113

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AT001	C	PRO	73	146,229	116,217	1,550	1.00	22.37	53
AT002	C	PRO	74	179,740	117,467	1,361	1.00	22.37	53
AT003	C	PRO	75	109,021	110,670	1,272	1.00	22.37	53
AT004	C	PRO	76	122,776	117,467	1,361	1.00	22.37	53
AT005	C	PRO	77	146,229	116,217	1,550	1.00	22.37	53
AT006	C	PRO	78	136,900	120,011	1,579	1.00	22.37	53
AT007	C	PRO	79	136,900	120,011	1,579	1.00	22.37	53
AT008	C	PRO	80	136,900	120,011	1,579	1.00	22.37	53
AT009	C	PRO	81	136,900	120,011	1,579	1.00	22.37	53
AT010	C	PRO	82	136,900	120,011	1,579	1.00	22.37	53
AT011	C	PRO	83	136,900	120,011	1,579	1.00	22.37	53
AT012	C	PRO	84	136,900	120,011	1,579	1.00	22.37	53
AT013	C	PRO	85	136,900	120,011	1,579	1.00	22.37	53
AT014	C	PRO	86	136,900	120,011	1,579	1.00	22.37	53
AT015	C	PRO	87	136,900	120,011	1,579	1.00	22.37	53
AT016	C	PRO	88	136,900	120,011	1,579	1.00	22.37	53
AT017	C	PRO	89	136,900	120,011	1,579	1.00	22.37	53
AT018	C	PRO	90	136,900	120,011	1,579	1.00	22.37	53
AT019	C	PRO	91	136,900	120,011	1,579	1.00	22.37	53
AT020	C	PRO	92	136,900	120,011	1,579	1.00	22.37	53
AT021	C	PRO	93	136,900	120,011	1,579	1.00	22.37	53
AT022	C	PRO	94	136,900	120,011	1,579	1.00	22.37	53
AT023	C	PRO	95	136,900	120,011	1,579	1.00	22.37	53
AT024	C	PRO	96	136,900	120,011	1,579	1.00	22.37	53
AT025	C	PRO	97	136,900	120,011	1,579	1.00	22.37	53
AT026	C	PRO	98	136,900	120,011	1,579	1.00	22.37	53
AT027	C	PRO	99	136,900	120,011	1,579	1.00	22.37	53
AT028	C	PRO	100	136,900	120,011	1,579	1.00	22.37	53
AT029	C	PRO	101	136,900	120,011	1,579	1.00	22.37	53
AT030	C	PRO	102	136,900	120,011	1,579	1.00	22.37	53
AT031	C	PRO	103	136,900	120,011	1,579	1.00	22.37	53
AT032	C	PRO	104	136,900	120,011	1,579	1.00	22.37	53
AT033	C	PRO	105	136,900	120,011	1,579	1.00	22.37	53
AT034	C	PRO	106	136,900	120,011	1,579	1.00	22.37	53
AT035	C	PRO	107	136,900	120,011	1,579	1.00	22.37	53
AT036	C	PRO	108	136,900	120,011	1,579	1.00	22.37	53
AT037	C	PRO	109	136,900	120,011	1,579	1.00	22.37	53
AT038	C	PRO	110	136,900	120,011	1,579	1.00	22.37	53
AT039	C	PRO	111	136,900	120,011	1,579	1.00	22.37	53
AT040	C	PRO	112	136,900	120,011	1,579	1.00	22.37	53
AT041	C	PRO	113	136,900	120,011	1,579	1.00	22.37	53
AT042	C	PRO	114	136,900	120,011	1,579	1.00	22.37	53
AT043	C	PRO	115	136,900	120,011	1,579	1.00	22.37	53
AT044	C	PRO	116	136,900	120,011	1,579	1.00	22.37	53
AT045	C	PRO	1						



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ATM 10403 C 700 74	274.391 125.399	20.543	1.00122.03	2710	ATM 11546 C 700 52	215.281 128.524	12.942	1.00 29.83	2770
ATM 10404 C 700 74	274.404 125.412	19.571	1.00122.03	2710	ATM 11547 C 700 52	215.224 128.765	12.233	1.00 29.83	2770
ATM 10405 C 700 74	274.417 125.425	19.571	1.00 31.19	2710	ATM 11548 C 700 52	215.061 129.006	11.515	1.00 29.83	2770
ATM 10406 C 700 74	274.430 125.438	19.571	1.00 31.19	2710	ATM 11549 C 700 52	214.898 129.247	10.797	1.00 29.83	2770
ATM 10407 C 700 74	274.443 125.451	19.571	1.00 31.19	2710	ATM 11550 C 700 52	214.735 129.488	10.079	1.00 29.83	2770
ATM 10408 C 700 74	274.456 125.464	19.571	1.00 31.19	2710	ATM 11551 C 700 52	214.572 129.729	9.361	1.00 29.83	2770
ATM 10409 C 700 74	274.469 125.477	19.571	1.00 31.19	2710	ATM 11552 C 700 52	214.409 129.970	8.643	1.00 29.83	2770
ATM 10410 C 700 74	274.482 125.490	19.571	1.00 31.19	2710	ATM 11553 C 700 52	214.246 130.211	7.925	1.00 29.83	2770
ATM 10411 C 700 74	274.495 125.503	19.571	1.00 31.19	2710	ATM 11554 C 700 52	214.083 130.452	7.207	1.00 29.83	2770
ATM 10412 C 700 74	274.508 125.516	19.571	1.00 31.19	2710	ATM 11555 C 700 52	213.920 130.693	6.489	1.00 29.83	2770
ATM 10413 C 700 74	274.521 125.529	19.571	1.00 31.19	2710	ATM 11556 C 700 52	213.757 130.934	5.771	1.00 29.83	2770
ATM 10414 C 700 74	274.534 125.542	19.571	1.00 31.19	2710	ATM 11557 C 700 52	213.594 131.175	5.053	1.00 29.83	2770
ATM 10415 C 700 74	274.547 125.555	19.571	1.00 31.19	2710	ATM 11558 C 700 52	213.431 131.416	4.335	1.00 29.83	2770
ATM 10416 C 700 74	274.560 125.568	19.571	1.00 31.19	2710	ATM 11559 C 700 52	213.268 131.657	3.617	1.00 29.83	2770
ATM 10417 C 700 74	274.573 125.581	19.571	1.00 31.19	2710	ATM 11560 C 700 52	213.105 131.898	2.899	1.00 29.83	2770
ATM 10418 C 700 74	274.586 125.594	19.571	1.00 31.19	2710	ATM 11561 C 700 52	212.942 132.139	2.181	1.00 29.83	2770
ATM 10419 C 700 74	274.599 125.607	19.571	1.00 31.19	2710	ATM 11562 C 700 52	212.779 132.380	1.463	1.00 29.83	2770
ATM 10420 C 700 74	274.612 125.620	19.571	1.00 31.19	2710	ATM 11563 C 700 52	212.616 132.621	0.745	1.00 29.83	2770
ATM 10421 C 700 74	274.625 125.633	19.571	1.00 31.19	2710	ATM 11564 C 700 52	212.453 132.862	0.027	1.00 29.83	2770
ATM 10422 C 700 74	274.638 125.646	19.571	1.00 31.19	2710	ATM 11565 C 700 52	212.290 133.103	-0.691	1.00 29.83	2770
ATM 10423 C 700 74	274.651 125.659	19.571	1.00 31.19	2710	ATM 11566 C 700 52	212.127 133.344	-1.409	1.00 29.83	2770
ATM 10424 C 700 74	274.664 125.672	19.571	1.00 31.19	2710	ATM 11567 C 700 52	211.964 133.585	-2.127	1.00 29.83	2770
ATM 10425 C 700 74	274.677 125.685	19.571	1.00 31.19	2710	ATM 11568 C 700 52	211.801 133.826	-2.845	1.00 29.83	2770
ATM 10426 C 700 74	274.690 125.698	19.571	1.00 31.19	2710	ATM 11569 C 700 52	211.638 134.067	-3.563	1.00 29.83	2770
ATM 10427 C 700 74	274.703 125.711	19.571	1.00 31.19	2710	ATM 11570 C 700 52	211.475 134.308	-4.281	1.00 29.83	2770
ATM 10428 C 700 74	274.716 125.724	19.571	1.00 31.19	2710	ATM 11571 C 700 52	211.312 134.549	-5.000	1.00 29.83	2770
ATM 10429 C 700 74	274.729 125.737	19.571	1.00 31.19	2710	ATM 11572 C 700 52	211.149 134.790	-5.718	1.00 29.83	2770
ATM 10430 C 700 74	274.742 125.750	19.571	1.00 31.19	2710	ATM 11573 C 700 52	210.986 135.031	-6.436	1.00 29.83	2770
ATM 10431 C 700 74	274.755 125.763	19.571	1.00 31.19	2710	ATM 11574 C 700 52	210.823 135.272	-7.154	1.00 29.83	2770
ATM 10432 C 700 74	274.768 125.776	19.571	1.00 31.19	2710	ATM 11575 C 700 52	210.660 135.513	-7.872	1.00 29.83	2770
ATM 10433 C 700 74	274.781 125.789	19.571	1.00 31.19	2710	ATM 11576 C 700 52	210.497 135.754	-8.590	1.00 29.83	2770
ATM 10434 C 700 74	274.794 125.802	19.571	1.00 31.19	2710	ATM 11577 C 700 52	210.334 135.995	-9.308	1.00 29.83	2770
ATM 10435 C 700 74	274.807 125.815	19.571	1.00 31.19	2710	ATM 11578 C 700 52	210.171 136.236	-10.026	1.00 29.83	2770
ATM 10436 C 700 74	274.820 125.828	19.571	1.00 31.19	2710	ATM 11579 C 700 52	210.008 136.477	-10.744	1.00 29.83	2770
ATM 10437 C 700 74	274.833 125.841	19.571	1.00 31.19	2710	ATM 11580 C 700 52	209.845 136.718	-11.462	1.00 29.83	2770
ATM 10438 C 700 74	274.846 125.854	19.571	1.00 31.19	2710	ATM 11581 C 700 52	209.682 136.959	-12.180	1.00 29.83	2770
ATM 10439 C 700 74	274.859 125.867	19.571	1.00 31.19	2710	ATM 11582 C 700 52	209.519 137.200	-12.898	1.00 29.83	2770
ATM 10440 C 700 74	274.872 125.880	19.571	1.00 31.19	2710	ATM 11583 C 700 52	209.356 137.441	-13.616	1.00 29.83	2770
ATM 10441 C 700 74	274.885 125.893	19.571	1.00 31.19	2710	ATM 11584 C 700 52	209.193 137.682	-14.334	1.00 29.83	2770
ATM 10442 C 700 74	274.898 125.906	19.571	1.00 31.19	2710	ATM 11585 C 700 52	209.030 137.923	-15.052	1.00 29.83	2770
ATM 10443 C 700 74	274.911 125.919	19.571	1.00 31.19	2710	ATM 11586 C 700 52	208.867 138.164	-15.770	1.00 29.83	2770
ATM 10444 C 700 74	274.924 125.932	19.571	1.00 31.19	2710	ATM 11587 C 700 52	208.704 138.405	-16.488	1.00 29.83	2770
ATM 10445 C 700 74	274.937 125.945	19.571	1.00 31.19	2710	ATM 11588 C 700 52	208.541 138.646	-17.206	1.00 29.83	2770
ATM 10446 C 700 74	274.950 125.958	19.571	1.00 31.19	2710	ATM 11589 C 700 52	208.378 138.887	-17.924	1.00 29.83	2770
ATM 10447 C 700 74	274.963 125.971	19.571	1.00 31.19	2710	ATM 11590 C 700 52	208.215 139.128	-18.642	1.00 29.83	2770
ATM 10448 C 700 74	274.976 125.984	19.571	1.00 31.19	2710	ATM 11591 C 700 52	208.052 139.369	-19.360	1.00 29.83	2770
ATM 10449 C 700 74	274.989 125.997	19.571	1.00 31.19	2710	ATM 11592 C 700 52	207.889 139.610	-20.078	1.00 29.83	2770
ATM 10450 C 700 74	275.002 126.010	19.571	1.00 31.19	2710	ATM 11593 C 700 52	207.726 139.851	-20.796	1.00 29.83	2770
ATM 10451 C 700 74	275.015 126.023	19.571	1.00 31.19	2710	ATM 11594 C 700 52	207.563 140.092	-21.514	1.00 29.83	2770
ATM 10452 C 700 74	275.028 126.036	19.571	1.00 31.19	2710	ATM 11595 C 700 52	207.400 140.333	-22.232	1.00 29.83	2770
ATM 10453 C 700 74	275.041 126.049	19.571	1.00 31.19	2710	ATM 11596 C 700 52	207.237 140.574	-22.950	1.00 29.83	2770
ATM 10454 C 700 74	275.054 126.062	19.571	1.00 31.19	2710	ATM 11597 C 700 52	207.074 140.815	-23.668	1.00 29.83	2770
ATM 10455 C 700 74	275.067 126.075	19.571	1.00 31.19	2710	ATM 11598 C 700 52	206.911 141.056	-24.386	1.00 29.83	2770
ATM 10456 C 700 74	275.080 126.088	19.571	1.00 31.19	2710	ATM 11599 C 700 52	206.748 141.297	-25.104	1.00 29.83	2770
ATM 10457 C 700 74	275.093 126.101	19.571	1.00 31.19	2710	ATM 11600 C 700 52	206.585 141.538	-25.822	1.00 29.83	2770
ATM 10458 C 700 74	275.106 126.114	19.571	1.00 31.19	2710	ATM 11601 C 700 52	206.422 141.779	-26.540	1.00 29.83	2770
ATM 10459 C 700 74	275.119 126.127	19.571	1.00 31.19	2710	ATM 11602 C 700 52	206.259 142.020	-27.258	1.00 29.83	2770
ATM 10460 C 700 74	275.132 126.140	19.571	1.00 31.19	2710	ATM 11603 C 700 52	206.096 142.261	-27.976	1.00 29.83	2770
ATM 10461 C 700 74	275.145 126.153	19.571	1.00 31.19	2710	ATM 11604 C 700 52	205.933 142.502	-28.694	1.00 29.83	2770
ATM 10462 C 700 74	275.158 126.166	19.571	1.00 31.19	2710	ATM 11605 C 700 52	205.770 142.743	-29.412	1.00 29.83	2770
ATM 10463 C 700 74	275.171 126.179	19.571	1.00 31.19	2710	ATM 11606 C 700 52	205.607 142.984	-30.130	1.00 29.83	2770
ATM 10464 C 700 74	275.184 126.192	19.571	1.00 31.19	2710	ATM 11607 C 700 52	205.444 143.225	-30.848	1.00 29.83	2770
ATM 10465 C 700 74	275.197 126.205	19.571	1.00 31.19	2710	ATM 11608 C 700 52	205.281 143.466	-31.566	1.00 29.83	2770
ATM 10466 C 700 74	275.210 126.218	19.571	1.00 31.19	2710	ATM 11609 C 700 52	205.118 143.707	-32.284	1.00 29.83	2770
ATM 10467 C 700 74	275.223 126.231	19.571	1.00 31.19	2710	ATM 11610 C 700 52	204.955 143.948	-33.002	1.00 29.83	2770
ATM 10468 C 700 74	275.236 126.244	19.571	1.00 31.19	2710	ATM 11611 C 700 52	204.792 144.189	-33.720	1.00 29.83	2770
ATM 10469 C 700 74	275.249 126.257	19.571	1.00 31.19	2710	ATM 11612 C 700 52	204.629 144.430	-34.438	1.00 29.83	2770
ATM 10470 C 700 74	275.262 126.270	19.571	1.00 31.19	2710	ATM 11613 C 700 52	204.466 144.671	-35.156	1.00 29.83	2770
ATM 10471 C 700 74	275.275 126.283	19.571	1.00 31.19	2710	ATM 11614 C 700 52	204.303 144.912	-35.874	1.00 29.83	2770
ATM 10472 C 700 74	275.288 126.296	19.571	1.00 31.19	2710	ATM 11615 C 700 52	204.140 145.153	-36.592	1.00 29.83	2770
ATM 10473 C 700 74	275.301 126.309	19.571	1.00 31.19	2710	ATM 11616 C 700 52	203.977 145.394	-37.310	1.00 29.83	2770
ATM 10474 C 700 74	275.314 126.322	19.571	1.00 31.19	2710	ATM 11617 C 700 52	203.814 145.635	-38.028	1.00 29.83	2770
ATM 10475 C 700 74	275.327 126.335	19.571	1.00 31.19	2710	ATM 11618 C 700 52	203.651 145.876	-38.746	1.00 29.83	2770
ATM 10476 C 700 74	275.340 126.348	19.571	1.00 31.19	2710	ATM 11619 C 700 52	203.488 146.117	-39.464	1.00 29.83	2770
ATM 10477 C 700 74	275.353 126.361	19.571	1.00 31.19	2710	ATM 11620 C 700 52	203.325 146.358	-40.182	1.00 29.83	2770
ATM 10478 C 700 74	275.366 126.374	19.571	1.00 31.19	2710	ATM 11621 C 700 52	203.162 146.599	-40.900	1.00 29.83	2770
ATM 10479 C 700 74	275.379 126.387	19.571	1.00 31.19	2710	ATM 11622 C 700 52	203.000 146.840	-41.618	1.00 29.83	2770
ATM 10480 C 700 74	275.392 126.400	19.571	1.00 31.19	2710	ATM 11623 C 700 52	202.837 147.081	-42.336		

ATCO	1001	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2310	ATCO	1122	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2311
ATCO	1002	HE	AM	00	261,943	168,000	18,700	1,801,777,33	2312	ATCO	1123	CA	ALA	00	218,190	146,214	36,912	1,001,97,00	2312
ATCO	1003	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2313	ATCO	1124	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2313
ATCO	1004	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2314	ATCO	1125	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2314
ATCO	1005	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2315	ATCO	1126	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2315
ATCO	1006	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2316	ATCO	1127	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2316
ATCO	1007	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2317	ATCO	1128	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2317
ATCO	1008	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2318	ATCO	1129	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2318
ATCO	1009	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2319	ATCO	1130	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2319
ATCO	1010	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2320	ATCO	1131	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2320
ATCO	1011	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2321	ATCO	1132	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2321
ATCO	1012	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2322	ATCO	1133	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2322
ATCO	1013	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2323	ATCO	1134	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2323
ATCO	1014	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2324	ATCO	1135	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2324
ATCO	1015	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2325	ATCO	1136	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2325
ATCO	1016	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2326	ATCO	1137	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2326
ATCO	1017	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2327	ATCO	1138	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2327
ATCO	1018	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2328	ATCO	1139	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2328
ATCO	1019	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2329	ATCO	1140	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2329
ATCO	1020	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2330	ATCO	1141	CA	ALA	00	210,727	146,214	31,007	1,002,012,00	2330
ATCO	1021	HE	AM	00	227,402	168,000	15,350	1,801,777,33	2331	ATCO	1142	CA	ALA	00	210,727	146,			

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AT20	12141	CA	MA	74	171.889	100.995	-84.881	1.00	43.43	706	AT20	12139	C	129	96	106.733	119.371	-79.311	1.00	34.12	706
AT20	12140	CA	MA	74	172.736	100.840	-83.552	1.00	17.18	706	AT20	12138	C	129	96	106.679	119.391	-77.552	1.00	34.12	706
AT20	12139	C	MA	74	172.892	100.717	-81.213	1.00	42.43	706	AT20	12137	C	129	96	106.625	119.411	-75.793	1.00	34.12	706
AT20	12138	C	MA	74	173.048	100.594	-78.974	1.00	42.43	706	AT20	12136	C	129	96	106.571	119.431	-74.034	1.00	34.12	706
AT20	12137	C	MA	74	173.204	100.471	-76.735	1.00	42.43	706	AT20	12135	C	129	96	106.517	119.451	-72.275	1.00	34.12	706
AT20	12136	C	MA	74	173.360	100.348	-74.496	1.00	42.43	706	AT20	12134	C	129	96	106.463	119.471	-70.516	1.00	34.12	706
AT20	12135	C	MA	74	173.516	100.225	-72.257	1.00	42.43	706	AT20	12133	C	129	96	106.409	119.491	-68.757	1.00	34.12	706
AT20	12134	C	MA	74	173.672	100.102	-70.018	1.00	42.43	706	AT20	12132	C	129	96	106.355	119.511	-67.000	1.00	34.12	706
AT20	12133	C	MA	74	173.828	100.000	-68.000	1.00	42.43	706	AT20	12131	C	129	96	106.301	119.531	-65.241	1.00	34.12	706
AT20	12132	C	MA	74	173.984	100.000	-66.000	1.00	42.43	706	AT20	12130	C	129	96	106.247	119.551	-63.482	1.00	34.12	706
AT20	12131	C	MA	74	174.140	100.000	-64.000	1.00	42.43	706	AT20	12129	C	129	96	106.193	119.571	-61.723	1.00	34.12	706
AT20	12130	C	MA	74	174.296	100.000	-62.000	1.00	42.43	706	AT20	12128	C	129	96	106.139	119.591	-59.964	1.00	34.12	706
AT20	12129	C	MA	74	174.452	100.000	-60.000	1.00	42.43	706	AT20	12127	C	129	96	106.085	119.611	-58.205	1.00	34.12	706
AT20	12128	C	MA	74	174.608	100.000	-58.000	1.00	42.43	706	AT20	12126	C	129	96	106.031	119.631	-56.446	1.00	34.12	706
AT20	12127	C	MA	74	174.764	100.000	-56.000	1.00	42.43	706	AT20	12125	C	129	96	105.977	119.651	-54.687	1.00	34.12	706
AT20	12126	C	MA	74	174.920	100.000	-54.000	1.00	42.43	706	AT20	12124	C	129	96	105.923	119.671	-52.928	1.00	34.12	706
AT20	12125	C	MA	74	175.076	100.000	-52.000	1.00	42.43	706	AT20	12123	C	129	96	105.869	119.691	-51.169	1.00	34.12	706
AT20	12124	C	MA	74	175.232	100.000	-50.000	1.00	42.43	706	AT20	12122	C	129	96	105.815	119.711	-49.410	1.00	34.12	706
AT20	12123	C	MA	74	175.388	100.000	-48.000	1.00	42.43	706	AT20	12121	C	129	96	105.761	119.731	-47.651	1.00	34.12	706
AT20	12122	C	MA	74	175.544	100.000	-46.000	1.00	42.43	706	AT20	12120	C	129	96	105.707	119.751	-45.892	1.00	34.12	706
AT20	12121	C	MA	74	175.700	100.000	-44.000	1.00	42.43	706	AT20	12119	C	129	96	105.653	119.771	-44.133	1.00	34.12	706
AT20	12120	C	MA	74	175.856	100.000	-42.000	1.00	42.43	706	AT20	12118	C	129	96	105.599	119.791	-42.374	1.00	34.12	706
AT20	12119	C	MA	74	176.012	100.000	-40.000	1.00	42.43	706	AT20	12117	C	129	96	105.545	119.811	-40.615	1.00	34.12	706
AT20	12118	C	MA	74	176.168	100.000	-38.000	1.00	42.43	706	AT20	12116	C	129	96	105.491	119.831	-38.856	1.00	34.12	706
AT20	12117	C	MA	74	176.324	100.000	-36.000	1.00	42.43	706	AT20	12115	C	129	96	105.437	119.851	-37.097	1.00	34.12	706
AT20	12116	C	MA	74	176.480	100.000	-34.000	1.00	42.43	706	AT20	12114	C	129	96	105.383	119.871	-35.338	1.00	34.12	706
AT20	12115	C	MA	74	176.636	100.000	-32.000	1.00	42.43	706	AT20	12113	C	129	96	105.329	119.891	-33.579	1.00	34.12	706
AT20	12114	C	MA	74	176.792	100.000	-30.000	1.00	42.43	706	AT20	12112	C	129	96	105.275	119.911	-31.820	1.00	34.12	706
AT20	12113	C	MA	74	176.948	100.000	-28.000	1.00	42.43	706	AT20	12111	C	129	96	105.221	119.931	-30.061	1.00	34.12	706
AT20	12112	C	MA	74	177.104	100.000	-26.000	1.00	42.43	706	AT20	12110	C	129	96	105.167	119.951	-28.302	1.00	34.12	706
AT20	12111	C	MA	74	177.260	100.000	-24.000	1.00	42.43	706	AT20	12109	C	129	96	105.113	119.971	-26.543	1.00	34.12	706
AT20	12110	C	MA	74	177.416	100.000	-22.000	1.00	42.43	706	AT20	12108	C	129	96	105.059	119.991	-24.784	1.00	34.12	706
AT20	12109	C	MA	74	177.572	100.000	-20.000	1.00	42.43	706	AT20	12107	C	129	96	105.005	120.011	-23.025	1.00	34.12	706
AT20	12108	C	MA	74	177.728	100.000	-18.000	1.00	42.43	706	AT20	12106	C	129	96	104.951	120.031	-21.266	1.00	34.12	706
AT20	12107	C	MA	74	177.884	100.000	-16.000	1.00	42.43	706	AT20	12105	C	129	96	104.897	120.051	-19.507	1.00	34.12	706
AT20	12106	C	MA	74	178.040	100.000	-14.000	1.00	42.43	706	AT20	12104	C	129	96	104.843	120.071	-17.748	1.00	34.12	706
AT20	12105	C	MA	74	178.196	100.000	-12.000	1.00	42.43	706	AT20	12103	C	129	96	104.789	120.091	-15.989	1.00	34.12	706
AT20	12104	C	MA	74	178.352	100.000	-10.000	1.00	42.43	706	AT20	12102	C	129	96	104.735	120.111	-14.230	1.00	34.12	706
AT20	12103	C	MA	74	178.508	100.000	-8.000	1.00	42.43	706	AT20	12101	C	129	96	104.681	120.131	-12.471	1.00	34.12	706
AT20	12102	C	MA	74	178.664	100.000	-6.000	1.00	42.43	706	AT20	12100	C	129	96	104.627	120.151	-10.712	1.00	34.12	706
AT20	12101	C	MA	74	178.820	100.000	-4.000	1.00	42.43	706	AT20	12099	C	129	96	104.573	120.171	-8.953	1.00	34.12	706
AT20	12100	C	MA	74	178.976	100.000	-2.000	1.00	42.43	706	AT20	12098	C	129	96	104.519	120.191	-7.194	1.00	34.12	706
AT20	12099	C	MA	74	179.132	100.000	0.000	1.00	42.43	706	AT20	12097	C	129	96	104.465	120.211	-5.435	1.00	34.12	706
AT20	12098	C	MA	74	179.288	100.000	2.000	1.00	42.43	706	AT20	12096	C	129	96	104.411	120.231	-3.676	1.00	34.12	706
AT20	12097	C	MA	74	179.444	100.000	4.000	1.00	42.43	706	AT20	12095	C	129	96	104.357	120.251	-1.917	1.00	34.12	706
AT20	12096	C	MA	74	179.600	100.000	6.000	1.00	42.43	706	AT20	12094	C	129	96	104.303	120.271	-0.158	1.00	34.12	706
AT20	12095	C	MA	74	179.756	100.000	8.000	1.00	42.43	706	AT20	12093	C	129	96	104.249	120.291	1.601	1.00	34.12	706
AT20	12094	C	MA	74	179.912	100.000	10.000	1.00	42.43	706	AT20	12092	C	129	96	104.195	120.311	3.362	1.00	34.12	706
AT20	12093	C	MA	74	180.068	100.000	12.000	1.00	42.43	706	AT20	12091	C	129	96	104.141	120.331	5.123	1.00	34.12	706
AT20	12092	C	MA	74	180.224	100.000	14.000	1.00	42.43	706	AT20	12090	C	129	96	104.087	120.351	6.884	1.00	34.12	706
AT20	12091	C	MA	74	180.380	100.000	16.000	1.00	42.43	706	AT20	12089	C	129	96	104.033	120.371	8.645	1.00	34.12	706
AT20	12090	C	MA	74	180.536	100.000	18.000	1.00	42.43	706	AT20	12088	C	129	96	103.979	120.391	10.406	1.00	34.12	706
AT20	12089	C	MA	74	180.692	100.000	20.000	1.00	42.43	706	AT20	12087	C	129	96	103.925	120.411	12.167	1.00	34.12	706
AT20	12088	C	MA	74	180.848	100.000	22.000	1.00	42.43	706	AT20	12086	C	129	96	103.871	120.431	13.928	1.00	34.12	706
AT20	12087	C	MA	74	181.004	100.000	24.000	1.00	42.43	706	AT20	12085	C	129	96	103.817	120.451	15.689	1.00	34.12	706
AT20	12086	C	MA	74	181.160	100.000	26.000	1.00	42.43	706	AT20	12084	C	129	96	103.763	120.471	17.450	1.00	34.12	706
AT20	12085	C	MA	74	181.316	100.000	28.000	1.00	42.43	706	AT20	12083	C	129	96	103.709	120.491	19.211	1.00	34.12	706
AT20	12084	C	MA	74	181.472	100.000	30.000	1.00	42.43	706	AT20	12082	C	129	96	103.655	120.511	20.972	1.00	34.12	706
AT20	12083	C	MA	74	181.628	100.000	32.000	1.00	42.43	706	AT20	12081	C	129	96	103.601	120.531	22.733	1.00	34.12	706
AT20	12082	C	MA	74	181.784	100.000	34.000	1.00	42.43	706	AT20	12080	C	129	96	103.547	120.551	24.494	1.00	34.12	706
AT20	12081	C	MA	74	181.940																



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ATCO	13500	C	AAA	207	184.138	103.713	-26.147	1.00	76.44	802
ATCO	13501	C	AAA	207	184.123	104.262	-28.086	1.00	76.44	802
ATCO	13502	C	AAA	207	184.104	105.279	-28.216	1.00	76.44	802
ATCO	13503	C	AAA	207	184.085	106.296	-28.345	1.00	76.44	802
ATCO	13504	C	AAA	207	184.066	107.313	-28.474	1.00	76.44	802
ATCO	13505	C	AAA	207	184.047	108.330	-28.603	1.00	76.44	802
ATCO	13506	C	AAA	207	184.028	109.347	-28.732	1.00	76.44	802
ATCO	13507	C	AAA	207	184.009	110.364	-28.861	1.00	76.44	802
ATCO	13508	C	AAA	207	183.990	111.381	-28.990	1.00	76.44	802
ATCO	13509	C	AAA	207	183.971	112.398	-29.119	1.00	76.44	802
ATCO	13510	C	AAA	207	183.952	113.415	-29.248	1.00	76.44	802
ATCO	13511	C	AAA	207	183.933	114.432	-29.377	1.00	76.44	802
ATCO	13512	C	AAA	207	183.914	115.449	-29.506	1.00	76.44	802
ATCO	13513	C	AAA	207	183.895	116.466	-29.635	1.00	76.44	802
ATCO	13514	C	AAA	207	183.876	117.483	-29.764	1.00	76.44	802
ATCO	13515	C	AAA	207	183.857	118.500	-29.893	1.00	76.44	802
ATCO	13516	C	AAA	207	183.838	119.517	-30.022	1.00	76.44	802
ATCO	13517	C	AAA	207	183.819	120.534	-30.151	1.00	76.44	802
ATCO	13518	C	AAA	207	183.800	121.551	-30.280	1.00	76.44	802
ATCO	13519	C	AAA	207	183.781	122.568	-30.409	1.00	76.44	802
ATCO	13520	C	AAA	207	183.762	123.585	-30.538	1.00	76.44	802
ATCO	13521	C	AAA	207	183.743	124.602	-30.667	1.00	76.44	802
ATCO	13522	C	AAA	207	183.724	125.619	-30.796	1.00	76.44	802
ATCO	13523	C	AAA	207	183.705	126.636	-30.925	1.00	76.44	802
ATCO	13524	C	AAA	207	183.686	127.653	-31.054	1.00	76.44	802
ATCO	13525	C	AAA	207	183.667	128.670	-31.183	1.00	76.44	802
ATCO	13526	C	AAA	207	183.648	129.687	-31.312	1.00	76.44	802
ATCO	13527	C	AAA	207	183.629	130.704	-31.441	1.00	76.44	802
ATCO	13528	C	AAA	207	183.610	131.721	-31.570	1.00	76.44	802
ATCO	13529	C	AAA	207	183.591	132.738	-31.699	1.00	76.44	802
ATCO	13530	C	AAA	207	183.572	133.755	-31.828	1.00	76.44	802
ATCO	13531	C	AAA	207	183.553	134.772	-31.957	1.00	76.44	802
ATCO	13532	C	AAA	207	183.534	135.789	-32.086	1.00	76.44	802
ATCO	13533	C	AAA	207	183.515	136.806	-32.215	1.00	76.44	802
ATCO	13534	C	AAA	207	183.496	137.823	-32.344	1.00	76.44	802
ATCO	13535	C	AAA	207	183.477	138.840	-32.473	1.00	76.44	802
ATCO	13536	C	AAA	207	183.458	139.857	-32.602	1.00	76.44	802
ATCO	13537	C	AAA	207	183.439	140.874	-32.731	1.00	76.44	802
ATCO	13538	C	AAA	207	183.420	141.891	-32.860	1.00	76.44	802
ATCO	13539	C	AAA	207	183.401	142.908	-32.989	1.00	76.44	802
ATCO	13540	C	AAA	207	183.382	143.925	-33.118	1.00	76.44	802
ATCO	13541	C	AAA	207	183.363	144.942	-33.247	1.00	76.44	802
ATCO	13542	C	AAA	207	183.344	145.959	-33.376	1.00	76.44	802
ATCO	13543	C	AAA	207	183.325	146.976	-33.505	1.00	76.44	802
ATCO	13544	C	AAA	207	183.306	147.993	-33.634	1.00	76.44	802
ATCO	13545	C	AAA	207	183.287	149.010	-33.763	1.00	76.44	802
ATCO	13546	C	AAA	207	183.268	150.027	-33.892	1.00	76.44	802
ATCO	13547	C	AAA	207	183.249	151.044	-34.021	1.00	76.44	802
ATCO	13548	C	AAA	207	183.230	152.061	-34.150	1.00	76.44	802
ATCO	13549	C	AAA	207	183.211	153.078	-34.279	1.00	76.44	802
ATCO	13550	C	AAA	207	183.192	154.095	-34.408	1.00	76.44	802
ATCO	13551	C	AAA	207	183.173	155.112	-34.537	1.00	76.44	802
ATCO	13552	C	AAA	207	183.154	156.129	-34.666	1.00	76.44	802
ATCO	13553	C	AAA	207	183.135	157.146	-34.795	1.00	76.44	802
ATCO	13554	C	AAA	207	183.116	158.163	-34.924	1.00	76.44	802
ATCO	13555	C	AAA	207	183.097	159.180	-35.053	1.00	76.44	802
ATCO	13556	C	AAA	207	183.078	160.197	-35.182	1.00	76.44	802
ATCO	13557	C	AAA	207	183.059	161.214	-35.311	1.00	76.44	802
ATCO	13558	C	AAA	207	183.040	162.231	-35.440	1.00	76.44	802
ATCO	13559	C	AAA	207	183.021	163.248	-35.569	1.00	76.44	802
ATCO	13560	C	AAA	207	183.002	164.265	-35.698	1.00	76.44	802
ATCO	13561	C	AAA	207	182.983	165.282	-35.827	1.00	76.44	802
ATCO	13562	C	AAA	207	182.964	166.299	-35.956	1.00	76.44	802
ATCO	13563	C	AAA	207	182.945	167.316	-36.085	1.00	76.44	802
ATCO	13564	C	AAA	207	182.926	168.333	-36.214	1.00	76.44	802
ATCO	13565	C	AAA	207	182.907	169.350	-36.343	1.00	76.44	802
ATCO	13566	C	AAA	207	182.888	170.367	-36.472	1.00	76.44	802
ATCO	13567	C	AAA	207	182.869	171.384	-36.601	1.00	76.44	802
ATCO	13568	C	AAA	207	182.850	172.401	-36.730	1.00	76.44	802
ATCO	13569	C	AAA	207	182.831	173.418	-36.859	1.00	76.44	802
ATCO	13570	C	AAA	207	182.812	174.435	-36.988	1.00	76.44	802
ATCO	13571	C	AAA	207	182.793	175.452	-37.117	1.00	76.44	802
ATCO	13572	C	AAA	207	182.774	176.469	-37.246	1.00	76.44	802
ATCO	13573	C	AAA	207	182.755	177.486	-37.375	1.00	76.44	802
ATCO	13574	C	AAA	207	182.736	178.503	-37.504	1.00	76.44	802
ATCO	13575	C	AAA	207	182.717	179.520	-37.633	1.00	76.44	802
ATCO	13576	C	AAA	207	182.698	180.537	-37.762	1.00	76.44	802
ATCO	13577	C	AAA	207	182.679	181.554	-37.891	1.00	76.44	802
ATCO	13578	C	AAA	207	182.660	182.571	-38.020	1.00	76.44	802
ATCO	13579	C	AAA	207	182.641	183.588	-38.149	1.00	76.44	802
ATCO	13580	C	AAA	207	182.622	184.605	-38.278	1.00	76.44	802
ATCO	13581	C	AAA	207	182.603	185.622	-38.407	1.00	76.44	802
ATCO	13582	C	AAA	207	182.584	186.639	-38.536	1.00	76.44	802
ATCO	13583	C	AAA	207	182.565	187.656	-38.665	1.00	76.44	802
ATCO	13584	C	AAA	207	182.546	188.673	-38.794	1.00	76.44	802
ATCO	13585	C	AAA	207	182.527	189.690	-38.923	1.00	76.44	802
ATCO	13586	C	AAA	207	182.508	190.707	-39.052	1.00	76.44	802
ATCO	13587	C	AAA	207	182.489	191.724	-39.181	1.00	76.44	802
ATCO	13588	C	AAA	207	182.470	192.741	-39.310	1.00	76.44	802
ATCO	13589	C	AAA	207	182.451	193.758	-39.439	1.00	76.44	802
ATCO	13590	C	AAA	207	182.432	194.775	-39.568	1.00	76.44	802
ATCO	13591	C	AAA	207	182.413	195.792	-39.697	1.00	76.44	802
ATCO	13592	C	AAA	207	182.394	196.809	-39.826	1.00	76.44	802
ATCO	13593	C	AAA	207	182.375	197.826	-39.955	1.00	76.44	802
ATCO	13594	C	AAA	207	182.356	198.843	-40.084	1.00	76.44	802
ATCO	13595	C	AAA	207	182.337	199.860	-40.213	1.00	76.44	802
ATCO	13596	C	AAA	207	182.318	200.877	-40.342	1.00	76.44	802
ATCO	13597	C	AAA	207	182.299	201.894	-40.471	1.00	76.44	802
ATCO	13598	C	AAA	207	182.280	202.911	-40.600	1.00	76.44	802
ATCO	13599	C	AAA	207	182.261	203.928	-40.729	1.00	76.44	802
ATCO	13600	C	AAA	207	182.242	204.945	-40.858	1.00	76.44	802
ATCO	13601	C	AAA	207	182.223	205.962	-40.987	1.00	76.44	802
ATCO	13602	C	AAA	207	182.204	206.979	-41.116	1.00	76.44	802
ATCO	13603	C	AAA	207	182.185	207.996	-41.245	1.00	76.44	802
ATCO	13604	C	AAA	207	182.166	209.013	-41.374	1.00	76.44	802
ATCO	13605	C	AAA	207	182.147	210.030	-41.503	1.00	76.44	802
ATCO	13606	C	AAA	207	182.128	211.047	-41.632	1.00	76.44	802
ATCO	13607	C	AAA	207	182.109	212.064	-41.761	1.00	76.44	802
ATCO	13608	C	AAA	207	182.090	213.081	-41.890	1.00	76.44	802
ATCO	13609	C	AAA	207	182.071	214.098	-42.019	1.00	76.44	802
ATCO	13610	C	AAA	207	182.052	215.115	-42.148	1.00	76.44	802
ATCO	13611	C	AAA	207	182.033	216.132	-42.277	1.00	76.44	802
ATCO	13612	C	AAA	207	182.014	217.149	-42.406	1.00	76.44	802
ATCO	13613	C	AAA	207	181.995	218.166	-42.535	1.00	76.44	802
ATCO	13614	C	AAA	207	181.976	219.183	-42.664	1.00	76.44	802
ATCO	13615	C	AAA	207	181.957	220.200	-42.793	1.00	76.44	802
ATCO	13616	C	AAA	207	181.938	221.217	-42.922	1.00	76.44	802
ATCO	13617	C	AAA	207	181.919	222.234	-43.051	1.00	76.44	802
ATCO	1361									

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ATCO 12321	C	AM	25	127.427	126.013	-14.371	1.00	29.76	200
ATCO 12322	C	AM	25	128.000	125.443	-14.511	1.00	30.76	200
ATCO 12323	C	AM	25	128.423	125.910	-14.509	1.00	31.76	200
ATCO 12324	C	AM	25	128.750	125.413	-15.337	1.00	32.76	200
ATCO 12325	C	AM	25	129.300	127.772	-22.528	1.00	33.76	200
ATCO 12326	C	AM	25	129.370	126.375	-22.995	1.00	34.76	200
ATCO 12327	C	AM	25	129.420	126.110	-23.310	1.00	35.76	200
ATCO 12328	C	AM	25	129.435	127.563	-18.872	1.00	36.76	200
ATCO 12329	C	AM	25	129.430	126.043	-23.387	1.00	37.76	200
ATCO 12330	C	AM	25	129.430	126.513	-26.843	1.00	38.76	200
ATCO 12331	C	AM	25	129.430	127.010	-21.027	1.00	39.76	200
ATCO 12332	C	AM	25	129.430	126.933	-21.770	1.00	40.76	200
ATCO 12333	C	AM	25	129.430	126.646	-26.340	1.00	41.76	200
ATCO 12334	C	AM	25	129.430	126.294	-26.972	1.00	42.76	200
ATCO 12335	C	AM	25	129.430	126.126	-26.850	1.00	43.76	200
ATCO 12336	C	AM	25	129.430	127.210	-21.229	1.00	44.76	200
ATCO 12337	C	AM	25	129.430	126.944	-26.312	1.00	45.76	200
ATCO 12338	C	AM	25	129.430	126.770	-26.346	1.00	46.76	200
ATCO 12339	C	AM	25	129.430	126.510	-26.904	1.00	47.76	200
ATCO 12340	C	AM	25	129.430	126.244	-26.944	1.00	48.76	200
ATCO 12341	C	AM	25	129.430	126.970	-21.065	1.00	49.76	200
ATCO 12342	C	AM	25	129.430	126.704	-26.366	1.00	50.76	200
ATCO 12343	C	AM	25	129.430	126.438	-26.904	1.00	51.76	200
ATCO 12344	C	AM	25	129.430	126.172	-26.944	1.00	52.76	200
ATCO 12345	C	AM	25	129.430	126.906	-21.085	1.00	53.76	200
ATCO 12346	C	AM	25	129.430	126.640	-26.386	1.00	54.76	200
ATCO 12347	C	AM	25	129.430	126.374	-26.926	1.00	55.76	200
ATCO 12348	C	AM	25	129.430	126.108	-26.966	1.00	56.76	200
ATCO 12349	C	AM	25	129.430	126.842	-21.127	1.00	57.76	200
ATCO 12350	C	AM	25	129.430	126.576	-26.368	1.00	58.76	200
ATCO 12351	C	AM	25	129.430	126.310	-26.408	1.00	59.76	200
ATCO 12352	C	AM	25	129.430	126.044	-26.448	1.00	60.76	200
ATCO 12353	C	AM	25	129.430	126.778	-21.129	1.00	61.76	200
ATCO 12354	C	AM	25	129.430	126.512	-26.488	1.00	62.76	200
ATCO 12355	C	AM	25	129.430	126.246	-26.528	1.00	63.76	200
ATCO 12356	C	AM	25	129.430	126.980	-21.169	1.00	64.76	200
ATCO 12357	C	AM	25	129.430	126.714	-26.568	1.00	65.76	200
ATCO 12358	C	AM	25	129.430	126.448	-26.608	1.00	66.76	200
ATCO 12359	C	AM	25	129.430	126.182	-26.648	1.00	67.76	200
ATCO 12360	C	AM	25	129.430	126.916	-21.189	1.00	68.76	200
ATCO 12361	C	AM	25	129.430	126.650	-26.688	1.00	69.76	200
ATCO 12362	C	AM	25	129.430	126.384	-26.728	1.00	70.76	200
ATCO 12363	C	AM	25	129.430	126.118	-26.768	1.00	71.76	200
ATCO 12364	C	AM	25	129.430	126.852	-21.231	1.00	72.76	200
ATCO 12365	C	AM	25	129.430	126.586	-26.768	1.00	73.76	200
ATCO 12366	C	AM	25	129.430	126.320	-26.808	1.00	74.76	200
ATCO 12367	C	AM	25	129.430	126.054	-26.848	1.00	75.76	200
ATCO 12368	C	AM	25	129.430	126.788	-21.273	1.00	76.76	200
ATCO 12369	C	AM	25	129.430	126.522	-26.888	1.00	77.76	200
ATCO 12370	C	AM	25	129.430	126.256	-26.928	1.00	78.76	200
ATCO 12371	C	AM	25	129.430	125.990	-26.968	1.00	79.76	200
ATCO 12372	C	AM	25	129.430	126.724	-21.315	1.00	80.76	200
ATCO 12373	C	AM	25	129.430	126.458	-26.968	1.00	81.76	200
ATCO 12374	C	AM	25	129.430	126.192	-27.008	1.00	82.76	200
ATCO 12375	C	AM	25	129.430	126.926	-21.357	1.00	83.76	200
ATCO 12376	C	AM	25	129.430	126.660	-27.048	1.00	84.76	200
ATCO 12377	C	AM	25	129.430	126.394	-27.088	1.00	85.76	200
ATCO 12378	C	AM	25	129.430	126.128	-27.128	1.00	86.76	200
ATCO 12379	C	AM	25	129.430	126.862	-21.405	1.00	87.76	200
ATCO 12380	C	AM	25	129.430	126.596	-27.168	1.00	88.76	200
ATCO 12381	C	AM	25	129.430	126.330	-27.208	1.00	89.76	200
ATCO 12382	C	AM	25	129.430	126.064	-27.248	1.00	90.76	200
ATCO 12383	C	AM	25	129.430	126.798	-21.447	1.00	91.76	200
ATCO 12384	C	AM	25	129.430	126.532	-27.288	1.00	92.76	200
ATCO 12385	C	AM	25	129.430	126.266	-27.328	1.00	93.76	200
ATCO 12386	C	AM	25	129.430	125.999	-27.368	1.00	94.76	200
ATCO 12387	C	AM	25	129.430	126.734	-21.489	1.00	95.76	200
ATCO 12388	C	AM	25	129.430	126.468	-27.408	1.00	96.76	200
ATCO 12389	C	AM	25	129.430	126.202	-27.448	1.00	97.76	200
ATCO 12390	C	AM	25	129.430	125.936	-27.488	1.00	98.76	200
ATCO 12391	C	AM	25	129.430	126.670	-21.529	1.00	99.76	200
ATCO 12392	C	AM	25	129.430	126.404	-27.528	1.00	100.76	200
ATCO 12393	C	AM	25	129.430	126.138	-27.568	1.00	101.76	200
ATCO 12394	C	AM	25	129.430	126.872	-21.571	1.00	102.76	200
ATCO 12395	C	AM	25	129.430	126.606	-27.608	1.00	103.76	200
ATCO 12396	C	AM	25	129.430	126.340	-27.648	1.00	104.76	200
ATCO 12397	C	AM	25	129.430	126.074	-27.688	1.00	105.76	200
ATCO 12398	C	AM	25	129.430	126.808	-21.629	1.00	106.76	200
ATCO 12399	C	AM	25	129.430	126.542	-27.728	1.00	107.76	200
ATCO 12400	C	AM	25	129.430	126.276	-27.768	1.00	108.76	200
ATCO 12401	C	AM	25	129.430	126.010	-27.808	1.00	109.76	200
ATCO 12402	C	AM	25	129.430	126.744	-21.671	1.00	110.76	200
ATCO 12403	C	AM	25	129.430	126.478	-27.848	1.00	111.76	200
ATCO 12404	C	AM	25	129.430	126.212	-27.888	1.00	112.76	200
ATCO 12405	C	AM	25	129.430	125.946	-27.928	1.00	113.76	200
ATCO 12406	C	AM	25	129.430	126.680	-21.713	1.00	114.76	200
ATCO 12407	C	AM	25	129.430	126.414	-27.968	1.00	115.76	200
ATCO 12408	C	AM	25	129.430	126.148	-28.008	1.00	116.76	200
ATCO 12409	C	AM	25	129.430	126.882	-21.755	1.00	117.76	200
ATCO 12410	C	AM	25	129.430	126.616	-28.048	1.00	118.76	200
ATCO 12411	C	AM	25	129.430	126.350	-28.088	1.00	119.76	200
ATCO 12412	C	AM	25	129.430	126.084	-28.128	1.00	120.76	200
ATCO 12413	C	AM	25	129.430	126.818	-21.801	1.00	121.76	200
ATCO 12414	C	AM	25	129.430	126.552	-28.168	1.00	122.76	200
ATCO 12415	C	AM	25	129.430	126.286	-28.208	1.00	123.76	200
ATCO 12416	C	AM	25	129.430	126.020	-28.248	1.00	124.76	200
ATCO 12417	C	AM	25	129.430	126.754	-21.843	1.00	125.76	200
ATCO 12418	C	AM	25	129.430	126.488	-28.288	1.00	126.76	200
ATCO 12419	C	AM	25	129.430	126.222	-28.328	1.00	127.76	200
ATCO 12420	C	AM	25	129.430	125.956	-28.368	1.00	128.76	200
ATCO 12421	C	AM	25	129.430	126.690	-21.885	1.00	129.76	200
ATCO 12422	C	AM	25	129.430	126.424	-28.408	1.00	130.76	200
ATCO 12423	C	AM	25	129.430	126.158	-28.448	1.00	131.76	200
ATCO 12424	C	AM	25	129.430	125.892	-28.488	1.00	132.76	200
ATCO 12425	C	AM	25	129.430	126.626	-21.921	1.00	133.76	200
ATCO 12426	C	AM	25	129.430	126.360	-28.528	1.00	134.76	200
ATCO 12427	C	AM	25	129.430	126.094	-28.568	1.00	135.76	200
ATCO 12428	C	AM	25	129.430	125.828	-28.608	1.00	136.76	200
ATCO 12429	C	AM	25	129.430	126.562	-21.955	1.00	137.76	200
ATCO 12430	C	AM	25	129.430	126.296	-28.648	1.00	138.76	200
ATCO 12431	C	AM	25	129.430	126.030	-28.688	1.00	139.76	200
ATCO 12432	C	AM	25	129.430	125.764	-28.728	1.00	140.76	200
ATCO 12433	C	AM	25	129.430	126.498	-21.991	1.00	141.76	200
ATCO 12434	C	AM	25	129.430	126.232	-28.768	1.00	142.76	200
ATCO 12435	C	AM	25	129.430	125.966	-28.808	1.00	143.76	200
ATCO 12436	C	AM	25	129.430	126.700	-22.029	1.00	144.76	200
ATCO 12437	C	AM	25	129.430	126.434	-28.848	1.00	145.76	200
ATCO 12438	C	AM	25	129.430	126.168	-28.888	1.00	146.76	200
ATCO 12439	C	AM	25	129.430	125.902	-28.928	1.00	147.76	200
ATCO 12440	C	AM	25	129.430	126.636	-22.061	1.00	148.76	200
ATCO 12441	C	AM	25	129.430	126.370	-28.968	1.00	149.76	200
ATCO 12442	C	AM	25	129.430	126.104	-29.008	1.00	150.76	200
ATCO 12443	C	AM	25	129.430	125.838	-29.048	1.00	151.76	200
ATCO 12444	C	AM	25	129.430</					

ATC01	10077	C	AME	60	175.95	124.99	-30.97	1.00	60.00	423	ATC01	10099	C	CLB	77	144.379	129.467	-14.912	1.00	70.75	424
ATC01	10078	C	AME	60	174.763	124.99	-30.775	1.00	60.00	423	ATC01	10091	C	CLB	77	144.304	124.262	-15.111	1.00	70.75	425
ATC01	10079	C	AME	60	175.950	127.210	-28.261	1.00	60.00	423	ATC01	10092	C	CLB	77	144.302	124.260	-14.799	1.00	70.75	426
ATC01	10080	C	AME	60	175.950	126.994	-28.956	1.00	60.00	423	ATC01	10093	C	CLB	77	144.301	124.259	-14.799	1.00	70.75	427
ATC01	10081	C	AME	60	174.773	127.210	-28.166	1.00	60.00	423	ATC01	10094	C	CLB	77	144.300	124.258	-14.799	1.00	70.75	428
ATC01	10082	C	AME	60	175.950	126.994	-28.956	1.00	60.00	423	ATC01	10095	C	CLB	77	144.300	124.257	-14.799	1.00	70.75	429
ATC01	10083	C	AME	60	175.950	126.994	-28.956	1.00	60.00	423	ATC01	10096	C	CLB	77	144.300	124.256	-14.799	1.00	70.75	430
ATC01	10084	C	AME	60	175.950	126.994	-28.956	1.00	60.00	423	ATC01	10097	C	CLB	77	144.300	124.255	-14.799	1.00	70.75	431
ATC01	10085	C	AME	60	175.950	126.994	-28.956	1.00	60.00	423	ATC01	10098	C	CLB	77	144.300	124.254	-14.799	1.00	70.75	432
ATC01	10086	C	AME	60	175.950	126.994	-28.956	1.00	60.00	423	ATC01	10099	C	CLB	77	144.300	124.253	-14.799	1.00	70.75	433
ATC01	10087	C	AME	60	175.950	126.994	-28.956	1.00	60.00	423	ATC01	10100	C	CLB	77	144.300	124.252	-14.799	1.00	70.75	434
ATC01	10088	C	AME	60	175.950	126.994	-28.956	1.00	60.00	423	ATC01	10101	C	CLB	77	144.300	124.251	-14.799	1.00	70.75	435
ATC01	10089	C	AME	60	175.950	126.994	-28.956	1.00	60.00	423	ATC01	10102	C	CLB	77	144.300	124.250	-14.799	1.00	70.75	436
ATC01	10090	C	AME	60	175.950	126.994	-28.956	1.00	60.00	423	ATC01	10103	C	CLB	77	144.300	124.249	-14.799	1.00	70.75	437
ATC01	10091	C	AME	60	175.950	126.994	-28.956	1.00	60.00	423	ATC01	10104	C	CLB	77	144.300	124.248	-14.799	1.00	70.75	438
ATC01	10092	C	AME	60	175.950	126.994	-28.956	1.00	60.00	423	ATC01	10105	C	CLB	77	144.300	124.247	-14.799	1.00	70.75	439
ATC01	10093	C	AME	60	175.950	126.994	-28.956	1.00	60.00	423	ATC01	10106	C	CLB	77	144.300	124.246	-14.799	1.00	70.75	440
ATC01	10094	C	AME	60	175.950	126.994	-28.956	1.00	60.00	423	ATC01	10107	C	CLB	77	144.300	124.245	-14.799	1.00	70.75	441
ATC01	10095	C	AME	60	175.950	126.994	-28.956	1.00	60.00	423	ATC01	10108	C	CLB	77	144.300	124.244	-14.799	1.00	70.75	442
ATC01	10096	C	AME	60	175.950	126.994	-28.956	1.00	60.00	423	ATC01	10109	C	CLB	77	144.300	124.243	-14.799	1.00	70.75	443
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AFN01	19943	01	CTT	179	99.470	99.742	-0.437	2.00	02.13	AL54
AFN02	12943	01	CTT	179	99.468	99.742	-0.499	2.00	02.13	AL55
AFN03	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL56
AFN04	19943	01	CTT	179	99.468	99.742	-0.499	2.00	02.13	AL57
AFN05	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL58
AFN06	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL59
AFN07	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL60
AFN08	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL61
AFN09	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL62
AFN10	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL63
AFN11	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL64
AFN12	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL65
AFN13	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL66
AFN14	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL67
AFN15	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL68
AFN16	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL69
AFN17	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL70
AFN18	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL71
AFN19	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL72
AFN20	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL73
AFN21	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL74
AFN22	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL75
AFN23	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL76
AFN24	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL77
AFN25	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL78
AFN26	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL79
AFN27	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL80
AFN28	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL81
AFN29	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL82
AFN30	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL83
AFN31	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL84
AFN32	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL85
AFN33	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL86
AFN34	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL87
AFN35	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL88
AFN36	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL89
AFN37	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL90
AFN38	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL91
AFN39	12943	01	CTT	179	99.470	99.742	-0.499	2.00	02.13	AL92</

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ATON 37065	C1	AMR	130	164,966	89,126	80,023	1,00	11.55	A150	ATON 37069	C1	AMR	136	156,991	83,799	1,147	1,00	46.47	A160
ATON 37066	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37070	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37067	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37071	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37068	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37072	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37069	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37073	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37070	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37074	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37071	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37075	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37072	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37076	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37073	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37077	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37074	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37078	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37075	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37079	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37076	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37080	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37077	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37081	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37078	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37082	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37079	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37083	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37080	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37084	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37081	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37085	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37082	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37086	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37083	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37087	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37084	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37088	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160
ATON 37085	C1	AMR	130	151,799	80,752	70,517	1,00	14.49	A150	ATON 37089	C1	AMR	136	151,113	82,772	1,279	1,00	46.47	A160</



















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[illegible]















172 of 182

[illegible]







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## TABLE 1B

TITLE STRUCTURE OF THE THERMAL POLYMERIZATION AND ECONOMIC EFFICIENCY

[illegible]

171	07	A	8	179,189	112,428	3,544	1,00	16,37
172	07	A	8	179,482	141,130	3,865	1,00	16,37
173	07	A	8	179,520	111,560	3,500	1,00	16,37
174	07	A	8	179,520	111,560	3,500	1,00	16,37
175	07	A	8	179,520	111,560	3,500	1,00	16,37
176	07	A	8	179,520	111,560	3,500	1,00	16,37
177	07	A	8	179,520	111,560	3,500	1,00	16,37
178	07	A	8	179,520	111,560	3,500	1,00	16,37
179	07	A	8	179,520	111,560	3,500	1,00	16,37
180	07	A	8	179,520	111,560	3,500	1,00	16,37
181	07	A	8	179,520	111,560	3,500	1,00	16,37
182	07	A	8	179,520	111,560	3,500	1,00	16,37
183	07	A	8	179,520	111,560	3,500	1,00	16,37
184	07	A	8	179,520	111,560	3,500	1,00	16,37
185	07	A	8	179,520	111,560	3,500	1,00	16,37
186	07	A	8	179,520	111,560	3,500	1,00	16,37
187	07	A	8	179,520	111,560	3,500	1,00	16,37
188	07	A	8	179,520	111,560	3,500	1,00	16,37
189	07	A	8	179,520	111,560	3,500	1,00	16,37
190	07	A	8	179,520	111,560	3,500	1,00	16,37
191	07	A	8	179,520	111,560	3,500	1,00	16,37
192	07	A	8	179,520	111,560	3,500	1,00	16,37
193	07	A	8	179,520	111,560	3,500	1,00	16,37
194	07	A	8	179,520	111,560	3,500	1,00	16,37
195	07	A	8	179,520	111,560	3,500	1,00	16,37
196	07	A	8	179,520	111,560	3,500	1,00	16,37
197	07	A	8	179,520	111,560	3,500	1,00	16,37
198	07	A	8	179,520	111,560	3,500	1,00	16,37
199	07	A	8	179,520	111,560	3,500	1,00	16,37
200	07	A	8	179,520	111,560	3,500	1,00	16,37
201	07	A	8	179,520	111,560	3,500	1,00	16,37
202	07	A	8	179,520	111,560	3,500	1,00	16,37
203	07	A	8	179,520	111,560	3,500	1,00	16,37
204	07	A	8	179,520	111,560	3,500	1,00	16,37
205	07	A	8	179,520	111,560	3,500	1,00	16,37
206	07	A	8	179,520	111,560	3,500	1,00	16,37
207	07	A	8	179,520	111,560	3,500	1,00	16,37
208	07	A	8	179,520	111,560	3,500	1,00	16,37
209	07	A	8	179,520	111,560	3,500	1,00	16,37
210	07	A	8	179,520	111,560	3,500	1,00	16,37
211	07	A	8	179,520	111,560	3,500	1,00	16,37
212	07	A	8	179,520	111,560	3,500	1,00	16,37
213	07	A	8	179,520	111,560	3,500	1,00	16,37
214	07	A	8	179,520	111,560	3,500	1,00	16,37
215	07	A	8	179,520	111,560	3,500	1,00	16,37
216	07	A	8	179,520	111,560	3,500	1,00	16,37
217	07	A	8	179,520	111,560	3,500	1,00	16,37
218	07	A	8	179,520	111,560	3,500	1,00	16,37
219	07	A	8	179,520	111,560	3,50		

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ATC01	164979	01	A	A	700	212.115	98.154	-72.991	1.00	55.29	
ATC01	164980	01	A	700	212.120	98.154	-72.991	1.00	55.29		
ATC01	164981	01	A	700	212.125	98.154	-72.991	1.00	55.29		
ATC01	164982	01	A	700	212.130	98.154	-72.991	1.00	55.29		
ATC01	164983	01	A	700	212.135	98.154	-72.991	1.00	55.29		
ATC01	164984	01	A	700	212.140	98.154	-72.991	1.00	55.29		
ATC01	164985	01	A	700	212.145	98.154	-72.991	1.00	55.29		
ATC01	164986	01	A	700	212.150	98.154	-72.991	1.00	55.29		
ATC01	164987	01	A	700	212.155	98.154	-72.991	1.00	55.29		
ATC01	164988	01	A	700	212.160	98.154	-72.991	1.00	55.29		
ATC01	164989	01	A	700	212.165	98.154	-72.991	1.00	55.29		
ATC01	164990	01	A	700	212.170	98.154	-72.991	1.00	55.29		
ATC01	164991	01	A	700	212.175	98.154	-72.991	1.00	55.29		
ATC01	164992	01	A	700	212.180	98.154	-72.991	1.00	55.29		
ATC01	164993	01	A	700	212.185	98.154	-72.991	1.00	55.29		
ATC01	164994	01	A	700	212.190	98.154	-72.991	1.00	55.29		
ATC01	164995	01	A	700	212.195	98.154	-72.991	1.00	55.29		
ATC01	164996	01	A	700	212.200	98.154	-72.991	1.00	55.29		
ATC01	164997	01	A	700	212.205	98.154	-72.991	1.00	55.29		
ATC01	164998	01	A	700	212.210	98.154	-72.991	1.00	55.29		
ATC01	164999	01	A	700	212.215	98.154	-72.991	1.00	55.29		
ATC01	165000	01	A	700	212.220	98.154	-72.991	1.00	55.29		
ATC01	165001	01	A	700	212.225	98.154	-72.991	1.00	55.29		
ATC01	165002	01	A	700	212.230	98.154	-72.991	1.00	55.29		
ATC01	165003	01	A	700	212.235	98.154	-72.991	1.00	55.29		
ATC01	165004	01	A	700	212.240	98.154	-72.991	1.00	55.29		
ATC01	165005	01	A	700	212.245	98.154	-72.991	1.00	55.29		
ATC01	165006	01	A	700	212.250	98.154	-72.991	1.00	55.29		
ATC01	165007	01	A	700	212.255	98.154	-72.991	1.00	55.29		
ATC01	165008	01	A	700	212.260	98.154	-72.991	1.00	55.29		
ATC01	165009	01	A	700	212.265	98.154	-72.991	1.00	55.29		
ATC01	165010	01	A	700	212.270	98.154	-72.991	1.00	55.29		
ATC01	165011	01	A	700	212.275	98.154	-72.991	1.00	55.29		
ATC01	165012	01	A	700	212.280	98.154	-72.991	1.00	55.29		
ATC01	165013	01	A	700	212.285	98.154	-72.991	1.00	55.29		
ATC01	165014	01	A	700	212.290	98.154	-72.991	1.00	55.29		
ATC01	165015	01	A	700	212.295	98.154	-72.991	1.00	55.29		
ATC01	165016	01	A	700	212.300	98.154	-72.991	1.00	55.29		
ATC01	165017	01	A	700	212.305	98.154	-72.991	1.00	55.29		
ATC01	165018	01	A	700	212.310	98.154	-72.991	1.00	55.29		
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ATCO 20404	02	C	A	770	236.136	116.730	31.932	1.00	34.42	C
ATCO 20405	03	C	A	770	279.822	126.743	39.407	1.00	34.42	C
ATCO 20406	04	C	A	770	275.704	127.835	38.180	1.00	34.42	C
ATCO 20407	05	C	A	770	276.401	128.712	37.719	1.00	34.42	C
ATCO 20408	06	C	A	770	228.915	119.939	27.124	1.00	34.42	C
ATCO 20409	07	C	A	770	246.626	124.759	27.939	1.00	34.42	C
ATCO 20410	08	C	A	770	235.790	122.132	28.124	1.00	34.42	C
ATCO 20411	09	C	A	770	277.811	126.245	37.219	1.00	34.42	C
ATCO 20412	10	C	A	770	231.901	121.600	26.950	1.00	34.42	C
ATCO 20413	11	C	A	770	231.900	122.600	28.124	1.00	34.42	C
ATCO 20414	12	C	A	770	279.433	127.870	38.232	1.00	34.42	C
ATCO 20415	13	C	A	770	273.245	124.563	36.201	1.00	34.42	C
ATCO 20416	14	C	A	770	227.802	118.266	25.879	1.00	34.42	C
ATCO 20417	15	C	A	770	238.078	126.995	37.735	1.00	34.42	C
ATCO 20418	16	C	A	770	226.728	117.777	26.526	1.00	34.42	C
ATCO 20419	17	C	A	770	276.343	126.177	37.817	1.00	34.42	C
ATCO 20420	18	C	A	770	280.133	127.878	38.026	1.00	34.42	C
ATCO 20421	19	C	A	770	277.843	126.730	37.329	1.00	34.42	C
ATCO 20422	20	C	A	770	232.708	127.823	37.948	1.00	34.42	C
ATCO 20423	21	C	A	770	232.707	128.796	37.978	1.00	34.42	C
ATCO 20424	22	C	A	770	232.706	129.769	37.999	1.00	34.42	C
ATCO 20425	23	C	A	770	232.705	130.742	38.019	1.00	34.42	C
ATCO 20426	24	C	A	770	232.704	131.715	38.039	1.00	34.42	C
ATCO 20427	25	C	A	770	232.703	132.688	38.059	1.00	34.42	C
ATCO 20428	26	C	A	770	232.702	133.661	38.079	1.00	34.42	C
ATCO 20429	27	C	A	770	232.701	134.634	38.099	1.00	34.42	C
ATCO 20430	28	C	A	770	232.700	135.607	38.119	1.00	34.42	C
ATCO 20431	29	C	A	770	232.699	136.580	38.139	1.00	34.42	C
ATCO 20432	30	C	A	770	232.698	137.553	38.159	1.00	34.42	C
ATCO 20433	31	C	A	770	232.697	138.526	38.179	1.00	34.42	C
ATCO 20434	32	C	A	770	232.696	139.499	38.199	1.00	34.42	C
ATCO 20435	33	C	A	770	232.695	140.472	38.219	1.00	34.42	C
ATCO 20436	34	C	A	770	232.694	141.445	38.239	1.00	34.42	C
ATCO 20437	35	C	A	770	232.693	142.418	38.259	1.00	34.42	C
ATCO 20438	36	C	A	770	232.692	143.391	38.279	1.00	34.42	C
ATCO 20439	37	C	A	770	232.691	144.364	38.299	1.00	34.42	C
ATCO 20440	38	C	A	770	232.690	145.337	38.319	1.00	34.42	C
ATCO 20441	39	C	A	770	232.689	146.310	38.339	1.00	34.42	C
ATCO 20442	40	C	A	770	232.688	147.283	38.359	1.00	34.42	C
ATCO 20443	41	C	A	770	232.687	148.256	38.379	1.00	34.42	C
ATCO 20444	42	C	A	770	232.686	149.229	38.399	1.00	34.42	C
ATCO 20445	43	C	A	770	232.685	150.202	38.419	1.00	34.42	C
ATCO 20446	44	C	A	770	232.684	151.175	38.439	1.00	34.42	C
ATCO 20447	45	C	A	770	232.683	152.148	38.459	1.00	34.42	C
ATCO 20448	46	C	A	770	232.682	153.121	38.479	1.00	34.42	C
ATCO 20449	47	C	A	770	232.681	154.094	38.499	1.00	34.42	C
ATCO 20450	48	C	A	770	232.680	155.067	38.519	1.00	34.42	C
ATCO 20451	49	C	A	770	232.679	156.040	38.539	1.00	34.42	C
ATCO 20452	50	C	A	770	232.678	157.013	38.559	1.00	34.42	C
ATCO 20453	51	C	A	770	232.677	157.986	38.579	1.00	34.42	C
ATCO 20454	52	C	A	770	232.676	158.959	38.599	1.00	34.42	C
ATCO 20455	53	C	A	770	232.675	159.932	38.619	1.00	34.42	C
ATCO 20456	54	C	A	770	232.674	160.905	38.639	1.00	34.42	C
ATCO 20457	55	C	A	770	232.673	161.878	38.659	1.00	34.42	C
ATCO 20458	56	C	A	770	232.672	162.851	38.679	1.00	34.42	C
ATCO 20459	57	C	A	770	232.671	163.824	38.699	1.00	34.42	C
ATCO 20460	58	C	A	770	232.670	164.797	38.719	1.00	34.42	C
ATCO 20461	59	C	A	770	232.669	165.770	38.739	1.00	34.42	C
ATCO 20462	60	C	A	770	232.668	166.743	38.759	1.00	34.42	C
ATCO 20463	61	C	A	770	232.667	167.716	38.779	1.00	34.42	C
ATCO 20464	62	C	A	770	232.666	168.689	38.799	1.00	34.42	C
ATCO 20465	63	C	A	770	232.665	169.662	38.819	1.00	34.42	C
ATCO 20466	64	C	A	770	232.664	170.635	38.839	1.00	34.42	C
ATCO 20467	65	C	A	770	232.663	171.608	38.859	1.00	34.42	C
ATCO 20468	66	C	A	770	232.662	172.581	38.879	1.00	34.42	C
ATCO 20469	67	C	A	770	232.661	173.554	38.899	1.00	34.42	C
ATCO 20470	68	C	A	770	232.660	174.527	38.919	1.00	34.42	C
ATCO 20471	69	C	A	770	232.659	175.500	38.939	1.00	34.42	C
ATCO 20472	70	C	A	770	232.658	176.473	38.959	1.00	34.42	C
ATCO 20473	71	C	A	770	232.657	177.446	38.979	1.00	34.42	C
ATCO 20474	72	C	A	770	232.656	178.419	38.999	1.00	34.42	C
ATCO 20475	73	C	A	770	232.655	179.392	39.019	1.00	34.42	C
ATCO 20476	74	C	A	770	232.654	180.365	39.039	1.00	34.42	C
ATCO 20477	75	C	A	770	232.653	181.338	39.059	1.00	34.42	C
ATCO 20478	76	C	A	770	232.652	182.311	39.079	1.00	34.42	C
ATCO 20479	77	C	A	770	232.651	183.284	39.099	1.00	34.42	C
ATCO 20480	78	C	A	770	232.650	184.257	39.119	1.00	34.42	C
ATCO 20481	79	C	A	770	232.649	185.230	39.139	1.00	34.42	C
ATCO 20482	80	C	A	770	232.648	186.203	39.159	1.00	34.42	C
ATCO 20483	81	C	A	770	232.647	187.176	39.179	1.00	34.42	C
ATCO 20484	82	C	A	770	232.646	188.149	39.199	1.00	34.42	C
ATCO 20485	83	C	A	770	232.645	189.122	39.219	1.00	34.42	C
ATCO 20486	84	C	A	770	232.644	190.095	39.239	1.00	34.42	C
ATCO 20487	85	C	A	770	232.643	191.068	39.259	1.00	34.42	C
ATCO 20488	86	C	A	770	232.642	192.041	39.279	1.00	34.42	C
ATCO 20489	87	C	A	770	232.641	193.014	39.299	1.00	34.42	C
ATCO 20490	88	C	A	770	232.640	193.987	39.319	1.00	34.42	C
ATCO 20491	89	C	A	770	232.639	194.960	39.339	1.00	34.42	C
ATCO 20492	90	C	A	770	232.638	195.933	39.359	1.00	34.42	C
ATCO 20493	91	C	A	770	232.637	196.906	39.379	1.00	34.42	C
ATCO 20494	92	C	A	770	232.636	197.879	39.399	1.00	34.42	C
ATCO 20495	93	C	A	770	232.635	198.852	39.419	1.00	34.42	C
ATCO 20496	94	C	A	770	232.634	199.825	39.439	1.00	34.42	C
ATCO 20497	95	C	A	770	232.633	200.798	39.459	1.00	34.42	C
ATCO 20498	96	C	A	770	232.632	201.771	39.479	1.00	34.42	C
ATCO 20499	97	C	A	770	232.631	202.744	39.499	1.00	34.42	C
ATCO 20500	98	C	A	770	232.630	203.717	39.519	1.00	34.42	C
ATCO 20501	99	C	A	770	232.629	204.690	39.539	1.00	34.42	C
ATCO 20502	100	C	A	770	232.628	205.663	39.559	1.00	34.42	C
ATCO 20503	101	C	A	770	232.627	206.636	39.579	1.00	34.42	C
ATCO 20504	102	C	A	770	232.626	207.609	39.599	1.00	34.42	C
ATCO 20505	103	C	A	770	232.625	208.582	39.619	1.00	34.42	C
ATCO 20506	104	C	A	770	232.624	209.555	39.639	1.00	34.42	C
ATCO 20507	105	C	A	770	232.623	210.528	39.659	1.00	34.42	C
ATCO 20508	106	C	A	770	232.622	211.501	39.679	1.00	34.42	C
ATCO 20509	107	C	A	770	232.621	212.474	39.699	1.00	34.42	C
ATCO 20510	108	C	A	770	232.620	213.447	39.719	1.00	34.42	C
ATCO 20511	109	C	A	770	232.619	214.420	39.739	1.00	34.42	C
ATCO 20512	110	C	A	770	232.618	215.393	39.759	1.00	34.42	C
ATCO 20513	111	C	A	770	232.617	216.366	39.779	1.00	34.42	C
ATCO 20514	112	C	A	770	232.616	217.339	39.799	1.00	34.42	C
ATCO 20515	113	C	A	770	232.615	218.312	39.819	1.00	34.42	C
ATCO 20516	114	C	A	770	232.614	219.285	39.839	1.00	34.42	C
ATCO 20517	115	C	A	770	232.613	220.258	39.859	1.00	34.42	C
ATCO 20518	116	C	A	770	232.612	221.231	39.879	1.00	34.42	C
ATCO 20519	117	C	A	770	232.611	222.204	39.899	1.00	34.42	C
ATCO 20520	118	C	A	770	232.610	223.177	39.919	1.00	34.42	C
ATCO 20521	119	C	A	770	232.609	224.150	39.939	1.00	34.42	C
ATCO 20522	120	C	A	770	232.608	225.123	39.959	1.00	34.42	C
ATCO 20523	121	C	A	770	232.607	226.096	39.979	1.00	34.42	C
ATCO 2052										

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ATM 12000 C2	0 A1110	236,647 842,992	7,140	1,00 14,26	C
ATM 12000 C3	0 A1110	237,362 841,869	7,179	1,00 14,26	C
ATM 12000 C4	0 A1110	238,077 840,746	7,218	1,00 14,26	C
ATM 12000 C5	0 A1110	238,792 839,623	7,257	1,00 14,26	C
ATM 12000 C6	0 A1110	239,507 838,500	7,296	1,00 14,26	C
ATM 12000 C7	0 A1110	240,222 837,377	7,335	1,00 14,26	C
ATM 12000 C8	0 A1110	240,937 836,254	7,374	1,00 14,26	C
ATM 12000 C9	0 A1110	241,652 835,131	7,413	1,00 14,26	C
ATM 12000 C10	0 A1110	242,367 834,008	7,452	1,00 14,26	C
ATM 12000 C11	0 A1110	243,082 832,885	7,491	1,00 14,26	C
ATM 12000 C12	0 A1110	243,797 831,762	7,530	1,00 14,26	C
ATM 12000 C13	0 A1110	244,512 830,639	7,569	1,00 14,26	C
ATM 12000 C14	0 A1110	245,227 829,516	7,608	1,00 14,26	C
ATM 12000 C15	0 A1110	245,942 828,393	7,647	1,00 14,26	C
ATM 12000 C16	0 A1110	246,657 827,270	7,686	1,00 14,26	C
ATM 12000 C17	0 A1110	247,372 826,147	7,725	1,00 14,26	C
ATM 12000 C18	0 A1110	248,087 825,024	7,764	1,00 14,26	C
ATM 12000 C19	0 A1110	248,802 823,901	7,803	1,00 14,26	C
ATM 12000 C20	0 A1110	249,517 822,778	7,842	1,00 14,26	C
ATM 12000 C21	0 A1110	250,232 821,655	7,881	1,00 14,26	C
ATM 12000 C22	0 A1110	250,947 820,532	7,920	1,00 14,26	C
ATM 12000 C23	0 A1110	251,662 819,409	7,959	1,00 14,26	C
ATM 12000 C24	0 A1110	252,377 818,286	7,998	1,00 14,26	C
ATM 12000 C25	0 A1110	253,092 817,163	8,037	1,00 14,26	C
ATM 12000 C26	0 A1110	253,807 816,040	8,076	1,00 14,26	C
ATM 12000 C27	0 A1110	254,522 814,917	8,115	1,00 14,26	C
ATM 12000 C28	0 A1110	255,237 813,794	8,154	1,00 14,26	C
ATM 12000 C29	0 A1110	255,952 812,671	8,193	1,00 14,26	C
ATM 12000 C30	0 A1110	256,667 811,548	8,232	1,00 14,26	C
ATM 12000 C31	0 A1110	257,382 810,425	8,271	1,00 14,26	C
ATM 12000 C32	0 A1110	258,097 809,302	8,310	1,00 14,26	C
ATM 12000 C33	0 A1110	258,812 808,179	8,349	1,00 14,26	C
ATM 12000 C34	0 A1110	259,527 807,056	8,388	1,00 14,26	C
ATM 12000 C35	0 A1110	260,242 805,933	8,427	1,00 14,26	C
ATM 12000 C36	0 A1110	260,957 804,810	8,466	1,00 14,26	C
ATM 12000 C37	0 A1110	261,672 803,687	8,505	1,00 14,26	C
ATM 12000 C38	0 A1110	262,387 802,564	8,544	1,00 14,26	C
ATM 12000 C39	0 A1110	263,102 801,441	8,583	1,00 14,26	C
ATM 12000 C40	0 A1110	263,817 800,318	8,622	1,00 14,26	C
ATM 12000 C41	0 A1110	264,532 799,195	8,661	1,00 14,26	C
ATM 12000 C42	0 A1110	265,247 798,072	8,700	1,00 14,26	C
ATM 12000 C43	0 A1110	265,962 796,949	8,739	1,00 14,26	C
ATM 12000 C44	0 A1110	266,677 795,826	8,778	1,00 14,26	C
ATM 12000 C45	0 A1110	267,392 794,703	8,817	1,00 14,26	C
ATM 12000 C46	0 A1110	268,107 793,580	8,856	1,00 14,26	C
ATM 12000 C47	0 A1110	268,822 792,457	8,895	1,00 14,26	C
ATM 12000 C48	0 A1110	269,537 791,334	8,934	1,00 14,26	C
ATM 12000 C49	0 A1110	270,252 790,211	8,973	1,00 14,26	C
ATM 12000 C50	0 A1110	270,967 789,088	9,012	1,00 14,26	C
ATM 12000 C51	0 A1110	271,682 787,965	9,051	1,00 14,26	C
ATM 12000 C52	0 A1110	272,397 786,842	9,090	1,00 14,26	C
ATM 12000 C53	0 A1110	273,112 785,719	9,129	1,00 14,26	C
ATM 12000 C54	0 A1110	273,827 784,596	9,168	1,00 14,26	C
ATM 12000 C55	0 A1110	274,542 783,473	9,207	1,00 14,26	C
ATM 12000 C56	0 A1110	275,257 782,350	9,246	1,00 14,26	C
ATM 12000 C57	0 A1110	275,972 781,227	9,285	1,00 14,26	C
ATM 12000 C58	0 A1110	276,687 780,104	9,324	1,00 14,26	C
ATM 12000 C59	0 A1110	277,402 778,981	9,363	1,00 14,26	C
ATM 12000 C60	0 A1110	278,117 777,858	9,402	1,00 14,26	C
ATM 12000 C61	0 A1110	278,832 776,735	9,441	1,00 14,26	C
ATM 12000 C62	0 A1110	279,547 775,612	9,480	1,00 14,26	C
ATM 12000 C63	0 A1110	280,262 774,489	9,519	1,00 14,26	C
ATM 12000 C64	0 A1110	280,977 773,366	9,558	1,00 14,26	C
ATM 12000 C65	0 A1110	281,692 772,243	9,597	1,00 14,26	C
ATM 12000 C66	0 A1110	282,407 771,120	9,636	1,00 14,26	C
ATM 12000 C67	0 A1110	283,122 770,000	9,675	1,00 14,26	C
ATM 12000 C68	0 A1110	283,837 768,875	9,714	1,00 14,26	C
ATM 12000 C69	0 A1110	284,552 767,750	9,753	1,00 14,26	C
ATM 12000 C70	0 A1110	285,267 766,625	9,792	1,00 14,26	C
ATM 12000 C71	0 A1110	285,982 765,500	9,831	1,00 14,26	C
ATM 12000 C72	0 A1110	286,697 764,375	9,870	1,00 14,26	C
ATM 12000 C73	0 A1110	287,412 763,250	9,909	1,00 14,26	C
ATM 12000 C74	0 A1110	288,127 762,125	9,948	1,00 14,26	C
ATM 12000 C75	0 A1110	288,842 761,000	9,987	1,00 14,26	C
ATM 12000 C76	0 A1110	289,557 759,875	10,026	1,00 14,26	C
ATM 12000 C77	0 A1110	290,272 758,750	10,065	1,00 14,26	C
ATM 12000 C78	0 A1110	290,987 757,625	10,104	1,00 14,26	C
ATM 12000 C79	0 A1110	291,702 756,500	10,143	1,00 14,26	C
ATM 12000 C80	0 A1110	292,417 755,375	10,182	1,00 14,26	C
ATM 12000 C81	0 A1110	293,132 754,250	10,221	1,00 14,26	C
ATM 12000 C82	0 A1110	293,847 753,125	10,260	1,00 14,26	C
ATM 12000 C83	0 A1110	294,562 752,000	10,299	1,00 14,26	C
ATM 12000 C84	0 A1110	295,277 750,875	10,338	1,00 14,26	C
ATM 12000 C85	0 A1110	295,992 749,750	10,377	1,00 14,26	C
ATM 12000 C86	0 A1110	296,707 748,625	10,416	1,00 14,26	C
ATM 12000 C87	0 A1110	297,422 747,500	10,455	1,00 14,26	C
ATM 12000 C88	0 A1110	298,137 746,375	10,494	1,00 14,26	C
ATM 12000 C89	0 A1110	298,852 745,250	10,533	1,00 14,26	C
ATM 12000 C90	0 A1110	299,567 744,125	10,572	1,00 14,26	C
ATM 12000 C91	0 A1110	300,282 743,000	10,611	1,00 14,26	C
ATM 12000 C92	0 A1110	300,997 741,875	10,650	1,00 14,26	C
ATM 12000 C93	0 A1110	301,712 740,750	10,689	1,00 14,26	C
ATM 12000 C94	0 A1110	302,427 739,625	10,728	1,00 14,26	C
ATM 12000 C95	0 A1110	303,142 738,500	10,767	1,00 14,26	C
ATM 12000 C96	0 A1110	303,857 737,375	10,806	1,00 14,26	C
ATM 12000 C97	0 A1110	304,572 736,250	10,845	1,00 14,26	C
ATM 12000 C98	0 A1110	305,287 735,125	10,884	1,00 14,26	C
ATM 12000 C99	0 A1110	306,002 734,000	10,923	1,00 14,26	C
ATM 12000 C100	0 A1110	306,717 732,875	10,962	1,00 14,26	C

AT00	24190	08	C	A1142	201,773	171,977	-29,804	1.00146,94	0	AT00	24423	C5	A1100	194,099	132,873	-71,097	1.00	75.44	E
AT00	24191	027	C	A1142	201,864	182,000	-19,864	1.00146,94	0	AT00	24424	06	A1100	194,079	132,800	-71,279	1.00	75.44	E
AT00	24192	00	C	A1142	201,900	176,101	-25,799	1.00146,94	0	AT00	24425	00	A1100	194,000	131,311	-72,689	1.00	75.44	E
AT00	24193	04	C	A1142	201,933	171,201	-30,732	1.00146,94	0	AT00	24426	C2	A1100	193,873	130,900	-72,923	1.00	75.44	E
AT00	24194	04	C	A1142	201,966	170,301	-31,665	1.00146,94	0	AT00	24427	03	A1100	193,753	130,201	-73,553	1.00	75.44	E
AT00	24195	07	C	A1142	201,999	169,401	-32,598	1.00146,94	0	AT00	24428	00	A1100	193,633	129,501	-74,183	1.00	75.44	E
AT00	24196	07	C	A1142	202,032	168,501	-33,531	1.00146,94	0	AT00	24429	00	A1100	193,513	128,801	-74,813	1.00	75.44	E
AT00	24197	07	C	A1142	202,065	167,601	-34,464	1.00146,94	0	AT00	24430	027	A1100	193,393	128,101	-75,443	1.00	75.44	E
AT00	24198	07	C	A1142	202,098	166,701	-35,397	1.00146,94	0	AT00	24431	00	A1100	193,273	127,401	-76,073	1.00	75.44	E
AT00	24199	07	C	A1142	202,131	165,801	-36,330	1.00146,94	0	AT00	24432	00	A1100	193,153	126,701	-76,703	1.00	75.44	E
AT00	24200	07	C	A1142	202,164	164,901	-37,263	1.00146,94	0	AT00	24433	00	A1100	193,033	126,001	-77,333	1.00	75.44	E
AT00	24201	07	C	A1142	202,197	164,001	-38,196	1.00146,94	0	AT00	24434	00	A1100	192,913	125,301	-77,963	1.00	75.44	E
AT00	24202	07	C	A1142	202,230	163,101	-39,129	1.00146,94	0	AT00	24435	00	A1100	192,793	124,601	-78,593	1.00	75.44	E
AT00	24203	07	C	A1142	202,263	162,201	-40,062	1.00146,94	0	AT00	24436	00	A1100	192,673	123,901	-79,223	1.00	75.44	E
AT00	24204	07	C	A1142	202,296	161,301	-40,995	1.00146,94	0	AT00	24437	00	A1100	192,553	123,201	-79,853	1.00	75.44	E
AT00	24205	07	C	A1142	202,329	160,401	-41,928	1.00146,94	0	AT00	24438	00	A1100	192,433	122,501	-80,483	1.00	75.44	E
AT00	24206	07	C	A1142	202,362	159,501	-42,861	1.00146,94	0	AT00	24439	00	A1100	192,313	121,801	-81,113	1.00	75.44	E
AT00	24207	07	C	A1142	202,395	158,601	-43,794	1.00146,94	0	AT00	24440	00	A1100	192,193	121,101	-81,743	1.00	75.44	E
AT00	24208	07	C	A1142	202,428	157,701	-44,727	1.00146,94	0	AT00	24441	00	A1100	192,073	120,401	-82,373	1.00	75.44	E
AT00	24209	07	C	A1142	202,461	156,801	-45,660	1.00146,94	0	AT00	24442	00	A1100	191,953	119,701	-83,003	1.00	75.44	E
AT00	24210	07	C	A1142	202,494	155,901	-46,593	1.00146,94	0	AT00	24443	00	A1100	191,833	119,001	-83,633	1.00	75.44	E
AT00	24211	07	C	A1142	202,527	155,001	-47,526	1.00146,94	0	AT00	24444	00	A1100	191,713	118,301	-84,263	1.00	75.44	E
AT00	24212	07	C	A1142	202,560	154,101	-48,459	1.00146,94	0	AT00	24445	00	A1100	191,593	117,601	-84,893	1.00	75.44	E
AT00	24213	07	C	A1142	202,593	153,201	-49,392	1.00146,94	0	AT00	24446	00	A1100	191,473	116,901	-85,523	1.00	75.44	E
AT00	24214	07	C	A1142	202,626	152,301	-50,325	1.00146,94	0	AT00	24447	00	A1100	191,353	116,201	-86,153	1.00	75.44	E
AT00	24215	07	C	A1142	202,659	151,401	-51,258	1.00146,94	0	AT00	24448	00	A1100	191,233	115,501	-86,783	1.00	75.44	E
AT00	24216	07	C	A1142	202,692	150,501	-52,191	1.00146,94	0	AT00	24449	00	A1100	191,113	114,801	-87,413	1.00	75.44	E
AT00	24217	07	C	A1142	202,725	149,601	-53,124	1.00146,94	0	AT00	24450	00	A1100	190,993	114,101	-88,043	1.00	75.44	E
AT00	24218	07	C	A1142	202,758	148,701	-54,057	1.00146,94	0	AT00	24451	00	A1100	190,873	113,401	-88,673	1.00	75.44	E
AT00	24219	07	C	A1142	202,791	147,801	-54,990	1.00146,94	0	AT00	24452	00	A1100	190,753	112,701	-89,303	1.00	75.44	E
AT00	24220	07	C	A1142	202,824	146,901	-55,923	1.00146,94	0	AT00	24453	00	A1100	190,633	112,001	-89,933	1.00	75.44	E
AT00	24221	07	C	A1142	202,857	146,001	-56,856	1.00146,94	0	AT00	24454	00	A1100	190,513	111,301	-90,563	1.00	75.44	E
AT00	24222	07	C	A1142	202,890	145,101	-57,789	1.00146,94	0	AT00	24455	00	A1100	190,393	110,601	-91,193	1.00	75.44	E
AT00	24223	07	C	A1142	202,923	144,201	-58,722	1.00146,94	0	AT00	24456	00	A1100	190,273	109,901	-91,823	1.00	75.44	E
AT00	24224	07	C	A1142	202,956	143,301	-59,655	1.00146,94	0	AT00	24457	00	A1100	190,153	109,201	-92,453	1.00	75.44	E
AT00	24225	07	C	A1142	202,989	142,401	-60,588	1.00146,94	0	AT00	24458	00	A1100	190,033	108,501	-93,083	1.00	75.44	E
AT00	24226	07	C	A1142	203,022	141,501	-61,521	1.00146,94	0	AT00	24459	00	A1100	189,913	107,801	-93,713	1.00	75.44	E
AT00	24227	07	C	A1142	203,055	140,601	-62,454	1.00146,94	0	AT00	24460	00	A1100	189,793	107,101	-94,343	1.00	75.44	E
AT00	24228	07	C	A1142	203,088	139,701	-63,387	1.00146,94	0	AT00	24461	00	A1100	189,673	106,401	-94,973	1.00	75.44	E
AT00	24229	07	C	A1142	203,121	138,801	-64,320	1.00146,94	0	AT00	24462	00	A1100	189,553	105,701	-95,603	1.00	75.44	E
AT00	24230	07	C	A1142	203,154	137,901	-65,253	1.00146,94	0	AT00	24463	00	A1100	189,433	105,001	-96,233	1.00	75.44	E
AT00	24231	07	C	A1142	203,187	137,001	-66,186	1.00146,94	0	AT00	24464	00	A1100	189,313	104,301	-96,863	1.00	75.44	E
AT00	24232	07	C	A1142	203,220	136,101	-67,119	1.00146,94	0	AT00	24465	00	A1100	189,193	103,601	-97,493	1.00	75.44	E
AT00	24233	07	C	A1142	203,253	135,201	-68,052	1.00146,94	0	AT00	24466	00	A1100	189,073	102,901	-98,123	1.00	75.44	E
AT00	24234	07	C	A1142	203,286	134,301	-68,985	1.00146,94	0	AT00	24467	00	A1100	188,953	102,201	-98,753	1.00	75.44	E
AT00	24235	07	C	A1142	203,319	133,401	-69,918	1.00146,94	0	AT00	24468	00	A1100	188,833	101,501	-99,383	1.00	75.44	E
AT00	24236	07	C	A1142	203,352	132,501	-70,851	1.00146,94	0	AT00	24469	00	A1100	188,713	100,801	-100,013	1.00	75.44	E
AT00	24237	07	C	A1142	203,385	131,601	-71,784	1.00146,94	0	AT00	24470	00	A1100	188,593	100,101	-100,643	1.00	75.44	E
AT00	24238	07	C	A1142	203,418	130,701	-72,717	1.00146,94	0	AT00	24471	00	A1100	188,473	99,401	-101,273	1.00	75.44	E
AT00	24239	07	C	A1142	203,451	129,801	-73,650	1.00146,94	0	AT00	24472	00	A1100	188,353	98,701	-101,903	1.00	75.44	E
AT00	24240	07	C	A1142	203,484	128,901	-74,583	1.00146,94	0	AT00	24473	00	A1100	188,233	98,001	-102,533	1.00	75.44	E
AT00	24241	07	C	A1142	203,517	128,001	-75,516	1.00146,94	0	AT00	24474	00	A1100	188,113	97,301	-103,163	1.00	75.44	E
AT00	24242	07	C	A1142	203,550	127,101	-76,449	1.00146,94	0	AT00	24475	00	A1100	187,993	96,601	-103,793	1.00	75.44	E
AT00	24243	07	C	A1142	203,583	126,201	-77,382	1.00146,94	0	AT00	24476	00	A1100	187,873	95,901	-104,423	1.00	75.44	E
AT00	24244	07	C	A1142	203,616	125,301	-78,315	1.00146,94	0	AT00	24477	00	A1100	187,753	95,201	-105,053	1.00	75.44	E
AT00	24245	07	C	A1142	203,649	124,401	-79,248	1.00146,94	0	AT00	24478	00	A1100	187,633	94,501	-105,683	1.00	75.44	E
AT00	24246	07	C	A1142	203,682	123,501	-80,181	1.00146,94	0	AT00	24479	00	A1100	187,513	93,801	-106,313	1.00	75.44	E
AT00	24247	07	C	A1142	203,715	122,601	-81,114	1.00146,94	0	AT00	24480	00	A1100	187,393	93,101	-106,943	1.00	75.44	E
AT00	24248	07	C	A1142	203,748	121,701	-82,047	1.00146,94	0	AT00	24481	00	A1100	187,273	92,401	-107,573	1.00	75.44	E
AT00	24249	07	C	A1142	203,781	120,801	-82,980	1.00146,94	0	AT00	24482	00	A1100	187,153	91,701	-108,203	1.00	75.44	E
AT00	24250	07	C	A1142	203,814	119,901	-83,913	1.00146,94	0	AT00	24483	00	A1100	187,033	91,001	-108,833	1.00	75.44	E
AT00	24251	07	C	A1142	203,847	119,001	-84,846	1.00146,94	0	AT00	24484	00	A1100	186,913	90,301	-109,463	1.00	75.44	E
AT00	24252	07	C	A1142	203,880	118,101	-85,779	1.00146,94	0	AT00	24485	00	A1100	186,793	89,601	-110,093	1.00	75.44	E
AT00	24253	07	C	A1142	203,913	117,201	-86,712	1.00146,94	0	AT00	24486</								









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ATON	30214	C	MA	25	194.537	112.979	45.025	1.00	52.56	C	ATON	30318	C	MA	25	170.452	112.919	36.793	1.00	52.56	C
ATON	30215	C	MA	25	195.520	112.977	47.000	1.00	52.59	C	ATON	30319	C	MA	25	170.452	112.919	36.793	1.00	52.56	C
ATON	30216	C	MA	25	196.503	112.975	48.975	1.00	52.63	C	ATON	30320	C	MA	25	171.435	112.917	38.768	1.00	52.59	C
ATON	30217	C	MA	25	197.486	112.973	50.950	1.00	52.67	C	ATON	30321	C	MA	25	172.418	112.915	40.743	1.00	52.62	C
ATON	30218	C	MA	25	198.469	112.971	52.925	1.00	52.71	C	ATON	30322	C	MA	25	173.401	112.913	42.718	1.00	52.65	C
ATON	30219	C	MA	25	199.452	112.969	54.900	1.00	52.75	C	ATON	30323	C	MA	25	174.384	112.911	44.693	1.00	52.68	C
ATON	30220	C	MA	25	200.435	112.967	56.875	1.00	52.79	C	ATON	30324	C	MA	25	175.367	112.909	46.668	1.00	52.72	C
ATON	30221	C	MA	25	201.418	112.965	58.850	1.00	52.83	C	ATON	30325	C	MA	25	176.350	112.907	48.643	1.00	52.75	C
ATON	30222	C	MA	25	202.401	112.963	60.825	1.00	52.87	C	ATON	30326	C	MA	25	177.333	112.905	50.618	1.00	52.79	C
ATON	30223	C	MA	25	203.384	112.961	62.800	1.00	52.91	C	ATON	30327	C	MA	25	178.316	112.903	52.593	1.00	52.82	C
ATON	30224	C	MA	25	204.367	112.959	64.775	1.00	52.95	C	ATON	30328	C	MA	25	179.299	112.901	54.568	1.00	52.86	C
ATON	30225	C	MA	25	205.350	112.957	66.750	1.00	52.99	C	ATON	30329	C	MA	25	180.282	112.899	56.543	1.00	52.89	C
ATON	30226	C	MA	25	206.333	112.955	68.725	1.00	53.03	C	ATON	30330	C	MA	25	181.265	112.897	58.518	1.00	53.03	C
ATON	30227	C	MA	25	207.316	112.953	70.700	1.00	53.07	C	ATON	30331	C	MA	25	182.248	112.895	60.493	1.00	53.07	C
ATON	30228	C	MA	25	208.299	112.951	72.675	1.00	53.11	C	ATON	30332	C	MA	25	183.231	112.893	62.468	1.00	53.11	C
ATON	30229	C	MA	25	209.282	112.949	74.650	1.00	53.15	C	ATON	30333	C	MA	25	184.214	112.891	64.443	1.00	53.15	C
ATON	30230	C	MA	25	210.265	112.947	76.625	1.00	53.19	C	ATON	30334	C	MA	25	185.197	112.889	66.418	1.00	53.19	C
ATON	30231	C	MA	25	211.248	112.945	78.600	1.00	53.23	C	ATON	30335	C	MA	25	186.180	112.887	68.393	1.00	53.23	C
ATON	30232	C	MA	25	212.231	112.943	80.575	1.00	53.27	C	ATON	30336	C	MA	25	187.163	112.885	70.368	1.00	53.27	C
ATON	30233	C	MA	25	213.214	112.941	82.550	1.00	53.31	C	ATON	30337	C	MA	25	188.146	112.883	72.343	1.00	53.31	C
ATON	30234	C	MA	25	214.197	112.939	84.525	1.00	53.35	C	ATON	30338	C	MA	25	189.129	112.881	74.318	1.00	53.35	C
ATON	30235	C	MA	25	215.180	112.937	86.500	1.00	53.39	C	ATON	30339	C	MA	25	190.112	112.879	76.293	1.00	53.39	C
ATON	30236	C	MA	25	216.163	112.935	88.475	1.00	53.43	C	ATON	30340	C	MA	25	191.095	112.877	78.268	1.00	53.43	C
ATON	30237	C	MA	25	217.146	112.933	90.450	1.00	53.47	C	ATON	30341	C	MA	25	192.078	112.875	80.243	1.00	53.47	C
ATON	30238	C	MA	25	218.129	112.931	92.425	1.00	53.51	C	ATON	30342	C	MA	25	193.061	112.873	82.218	1.00	53.51	C
ATON	30239	C	MA	25	219.112	112.929	94.400	1.00	53.55	C	ATON	30343	C	MA	25	194.044	112.871	84.193	1.00	53.55	C
ATON	30240	C	MA	25	220.095	112.927	96.375	1.00	53.59	C	ATON	30344	C	MA	25	195.027	112.869	86.168	1.00	53.59	C
ATON	30241	C	MA	25	221.078	112.925	98.350	1.00	53.63	C	ATON	30345	C	MA	25	196.010	112.867	88.143	1.00	53.63	C
ATON	30242	C	MA	25	222.061	112.923	100.325	1.00	53.67	C	ATON	30346	C	MA	25	196.993	112.865	90.118	1.00	53.67	C
ATON	30243	C	MA	25	223.044	112.921	102.300	1.00	53.71	C	ATON	30347	C	MA	25	197.976	112.863	92.093	1.00	53.71	C
ATON	30244	C	MA	25	224.027	112.919	104.275	1.00	53.75	C	ATON	30348	C	MA	25	198.959	112.861	94.068	1.00	53.75	C
ATON	30245	C	MA	25	225.010	112.917	106.250	1.00	53.79	C	ATON	30349	C	MA	25	199.942	112.859	96.043	1.00	53.79	C
ATON	30246	C	MA	25	225.993	112.915	108.225	1.00	53.83	C	ATON	30350	C	MA	25	200.925	112.857	98.018	1.00	53.83	C
ATON	30247	C	MA	25	226.976	112.913	110.200	1.00	53.87	C	ATON	30351	C	MA	25	201.908	112.855	100.000	1.00	53.87	C
ATON	30248	C	MA	25	227.959	112.911	112.175	1.00	53.91	C	ATON	30352	C	MA	25	202.891	112.853	101.975	1.00	53.91	C
ATON	30249	C	MA	25	228.942	112.909	114.150	1.00	53.95	C	ATON	30353	C	MA	25	203.874	112.851	103.950	1.00	53.95	C
ATON	30250	C	MA	25	229.925	112.907	116.125	1.00	53.99	C	ATON	30354	C	MA	25	204.857	112.849	105.925	1.00	53.99	C
ATON	30251	C	MA	25	230.908	112.905	118.100	1.00	54.03	C	ATON	30355	C	MA	25	205.840	112.847	107.900	1.00	54.03	C
ATON	30252	C	MA	25	231.891	112.903	120.075	1.00	54.07	C	ATON	30356	C	MA	25	206.823	112.845	109.875	1.00	54.07	C
ATON	30253	C	MA	25	232.874	112.901	122.050	1.00	54.11	C	ATON	30357	C	MA	25	207.806	112.843	111.850	1.00	54.11	C
ATON	30254	C	MA	25	233.857	112.899	124.025	1.00	54.15	C	ATON	30358	C	MA	25	208.789	112.841	113.825	1.00	54.15	C
ATON	30255	C	MA	25	234.840	112.897	126.000	1.00	54.19	C	ATON	30359	C	MA	25	209.772	112.839	115.800	1.00	54.19	C
ATON	30256	C	MA	25	235.823	112.895	127.975	1.00	54.23	C	ATON	30360	C	MA	25	210.755	112.837	117.775	1.00	54.23	C
ATON	30257	C	MA	25	236.806	112.893	129.950	1.00	54.27	C	ATON	30361	C	MA	25	211.738	112.835	119.750	1.00	54.27	C
ATON	30258	C	MA	25	237.789	112.891	131.925	1.00	54.31	C	ATON	30362	C	MA	25	212.721	112.833	121.725	1.00	54.31	C
ATON	30259	C	MA	25	238.772	112.889	133.900	1.00	54.35	C	ATON	30363	C	MA	25	213.704	112.831	123.700	1.00	54.35	C
ATON	30260	C	MA	25	239.755	112.887	135.875	1.00	54.39	C	ATON	30364	C	MA	25	214.687	112.829	125.675	1.00	54.39	C
ATON	30261	C	MA	25	240.738	112.885	137.850	1.00	54.43	C	ATON	30365	C	MA	25	215.670	112.827	127.650	1.00	54.43	C
ATON	30262	C	MA	25	241.721	112.883	139.825	1.00	54.47	C	ATON	30366	C	MA	25	216.653	112.825	129.625	1.00	54.47	C
ATON	30263	C	MA	25	242.704	112.881	141.800	1.00	54.51	C	ATON	30367	C	MA	25	217.636	112.823	131.600	1.00	54.51	C
ATON	30264	C	MA	25	243.687	112.879	143.775	1.00	54.55	C	ATON	30368	C	MA	25	218.619	112.821	133.575	1.00	54.55	C
ATON	30265	C	MA	25	244.670	112.877	145.750	1.00	54.59	C	ATON	30369	C	MA	25	219.602	112.819	135.550	1.00	54.59	C
ATON	30266	C	MA	25	245.653	112.875	147.725	1.00	54.63	C	ATON	30370	C	MA	25	220.585	112.817	137.525	1.00	54.63	C
ATON	30267	C	MA	25	246.636	112.873	149.700	1.00	54.67	C	ATON	30371	C	MA	25	221.568	112.815	139.500	1.00	54.67	C
ATON	30268	C	MA	25	247.619	112.871	151.675	1.00	54.71	C	ATON	30372	C	MA	25	222.551	112.813	141.475	1.00	54.71	C
ATON	30269	C	MA	25	248.602	112.869	153.650	1.00	54.75	C	ATON	30373	C	MA	25	223.534	112.811	143.450	1.00	54.75	C
ATON	30270	C	MA	25	249.585	112.867	155.625	1.00	54.79	C	ATON	30374	C	MA	25	224.517	112.809	145.425	1.00	54.79	C
ATON	30271	C	MA	25	250.568	112.865	157.600	1.00	54.83	C	ATON	30375	C	MA	25	225.500	112.807	147.400	1.00	54.83	C
ATON	30272	C	MA	25	251.551	112.863	159.575	1.00	54.87	C	ATON	30376	C	MA	25	226.483	112.805	149.375	1.00	54.87	C
ATON	30273	C	MA	25	252.534	112.861	161.550	1.00	54.91	C	ATON	30377	C	MA	25	227.466	112.803	151.350	1.00	54.91	C
ATON	30274	C	MA	25	253.517	112.859	163.525	1.00	54.95	C	ATON	30378	C	MA	25	228.449	112.801	153.325	1.00	54.95	C
ATON	30275	C	MA	25	254.500	112.857	165.500	1.00	54.99	C	ATON	30379	C	MA	25	229.432	112.799	155.300	1.00	54.99	C
ATON	30276	C	MA	25	255.483	112.855	167.475	1.00	55.03	C	ATON	30380	C	MA	25	230.415	112.797	157.275	1.00	55.03	C
ATON	30277	C	MA	25	256.466																

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**Fig.**

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ATC01	42137	C	612	0	110	227,040	112,705	-1,493	1,00	11,70
ATC01	42138	C	612	0	110	227,045	112,707	-1,493	1,00	11,70
ATC01	42139	C	612	0	110	227,050	112,709	-1,493	1,00	11,70
ATC01	42140	C	612	0	110	227,055	112,711	-1,493	1,00	11,70
ATC01	42141	C	612	0	110	227,060	112,713	-1,493	1,00	11,70
ATC01	42142	C	612	0	110	227,065	112,715	-1,493	1,00	11,70
ATC01	42143	C	612	0	110	227,070	112,717	-1,493	1,00	11,70
ATC01	42144	C	612	0	110	227,075	112,719	-1,493	1,00	11,70
ATC01	42145	C	612	0	110	227,080	112,721	-1,493	1,00	11,70
ATC01	42146	C	612	0	110	227,085	112,723	-1,493	1,00	11,70
ATC01	42147	C	612	0	110	227,090	112,725	-1,493	1,00	11,70
ATC01	42148	C	612	0	110	227,095	112,727	-1,493	1,00	11,70
ATC01	42149	C	612	0	110	227,100	112,729	-1,493	1,00	11,70
ATC01	42150	C	612	0	110	227,105	112,731	-1,493	1,00	11,70
ATC01	42151	C	612	0	110	227,110	112,733	-1,493	1,00	11,70
ATC01	42152	C	612	0	110	227,115	112,735	-1,493	1,00	11,70
ATC01	42153	C	612	0	110	227,120	112,737	-1,493	1,00	11,70
ATC01	42154	C	612	0	110	227,125	112,739	-1,493	1,00	11,70
ATC01	42155	C	612	0	110	227,130	112,741	-1,493	1,00	11,70
ATC01	42156	C	612	0	110	227,135	112,743	-1,493	1,00	11,70
ATC01	42157	C	612	0	110	227,140	112,745	-1,493	1,00	11,70
ATC01	42158	C	612	0	110	227,145	112,747	-1,493	1,00	11,70
ATC01	42159	C	612	0	110	227,150	112,749	-1,493	1,00	11,70
ATC01	42160	C	612	0	110	227,155	112,751	-1,493	1,00	11,70
ATC01	42161	C	612	0	110	227,160	112,753	-1,493	1,00	11,70
ATC01	42162	C	612	0	110	227,165	112,755	-1,493	1,00	11,70
ATC01	42163	C	612	0	110	227,170	112,757	-1,493	1,00	11,70
ATC01	42164	C	612	0	110	227,175	112,759	-1,493	1,00	11,70
ATC01	42165	C	612	0	110	227,180	112,761	-1,493	1,00	11,70
ATC01	42166	C	612	0	110	227,185	112,763	-1,493	1,00	11,70
ATC01	42167	C	612	0	110	227,190	112,765	-1,493	1,00	11,70
ATC01	42168	C	612	0	110	227,195	112,767	-1,493	1,00	11,70
ATC01	42169	C	612	0	110	227,200	112,769	-1,493	1,00	11,70
ATC01	42170	C	612	0	110	227,205	112,771	-1,493	1,00	11,70
ATC01	42171	C	612	0	110	227,210	112,773	-1,493	1,00	11,70
ATC01	42172	C	612	0	110	227,215	112,775	-1,493	1,00	11,70
ATC01	42173	C	612	0	110	227,220	112,777	-1,493	1,00	11,70
ATC01	42174	C	612	0	110	227,225	112,779	-1,493	1,00	11,70
ATC01	42175	C	612	0	110	227,230	112,781	-1,493	1,00	11,70
ATC01	42176	C	612							





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NETWTS1946	WWE	WWE	180	195.977	95.902	-29.819	0.33	50.49	X
NETWTS1947	WWE	WWE	200	196.601	104.500	-13.777	0.30	53.66	X
NETWTS1948	WWE	WWE	201	191.529	108.100	-13.133	0.44	53.66	X
NETWTS1949	WWE	WWE	202	186.202	151.757	-71.100	0.45	50.49	X
CHAPTER	1179	0	190	00	09	0	0	634927	22
END									0 323



European Patent  
Office

## EUROPEAN SEARCH REPORT

Application Number  
EP 01 30 6060

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
Y,D	CLEMONS JR ET AL: "Structure of a bacterial 30S ribosomal subunit at 5.5 Å resolution" NATURE, vol. 400, 26 August 1999 (1999-08-26), pages 833-840, XP002182367 * See page 833 (3.6 Å), page 836 (Figure 3) and pages 838-839 (Discussion) *	1,2	C07K14/195 G06F17/50
Y,D	TOCILJ ET AL: "The small ribosomal subunit from Thermus thermophilus at 4.5 Å resolution: Pattern fittings and the identification of a functional site" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES, USA, vol. 96, 7 December 1999 (1999-12-07), pages 14252-14257, XP002182368 * See page 14253 (Table 1) *	1,2	
A	AGALAROV ET AL: "Structure of the S15,S6,S18-rRNA complex: Assembly of the 30S ribosome central domain" SCIENCE, vol. 288, 7 April 2000 (2000-04-07), pages 107-112, XP002182369 * See page 108 (Figure 1 and Table 1) *	1-11	TECHNICAL FIELDS SEARCHED (Int.Cl.7)  C07K G06F
P,X	WIMBERLY: "Structure of the 30S ribosomal subunit" NATURE, vol. 407, 21 September 2000 (2000-09-21), pages 327-339, XP002182370 * See page 332 (Figure 5) and 335 (Table 2) *	1-11	
The present search report has been drawn up for all claims			
Place of search <b>BERLIN</b>		Date of completion of the search <b>13 November 2001</b>	Examiner <b>Korsner, S-E</b>
CATEGORY OF CITED DOCUMENTS X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document			

EPO FORM 1603 (03-02) (P04C01)

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